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l		MENT OF COMMERCE PATENT AND TRADEMARK	OFFICE	ATTORNEY DOCKET NO. P07180ÚS00/BAS
l		ER TO THE UNITED STATES	-	U.S. APPLICATION NO.
١		CTED OFFICE (DO/EO/US)		The state of the s
L		LING UNDER 35 U.S.C. 371		0978378433
l	INTERNATIONAL APPLICATION NO. PCT/FR99/02643	INTERNATIONAL FILING DÂTE 28 October 1999	PRI	ORITY DATE CLAIMED 30 October 1998
İ	TITLE OF INVENTION: NUCLEIC ACI		OF THE N	
ŀ	APPLICANT(S) FOR DO/EO/US: AUJAM			
ł	Applicant herewith submits to the US Design		ing items an	nd other information:
l		,	_	a outer information.
l	·	items concerning a filing under 35 U.S.O		•
l		QUENT submission of items concerning	_	
	examination until the expiration	ational examination procedures (35 USC n of the applicable time limit set in 35 USC and Preliminary Examination was made	SC 371(b)	and PCT Art. 22 and 39(1).
l	claimed priority date.	plication as filed (35 U.S.C. 371 (c)(2))	•	
l	<u> </u>	quired only if not transmitted by the Inter	rnational B	? ?urequ)
l	X b. has been transmitted by the		mational L	ourcauj.
l	_	ication was filed in the United States Rec	eiving Off	fice (RO/US)
l	-	nal Application into English (35 U.S.C. 3	_	·
l		he International Appln. under PCT Articl		
l		equired only if not transmitted by the Int	•	
I	b. have been transmitted by the		011101101101	20.000).
l	<u> </u>	ver, the time limit for making such amen	dments ha	d NOT expired.
ļ	d. have not been made and w			arior inpired.
١			TICC 2	71(~)(2))
١		ts to the claims under PCT Article 19 (35	0.S.C. 3	/1(c)(3)).
١	9. An oath or declaration of the in		T A -41-1- 0	0.C (2.E II 0.C. 271(-)(E))
		the Int'l Prelim. Exam. Report under PC	1 Article 3	36 (33 U.S.C. 3/1(c)(3)).
ı	items 11. to 20. below concern do	cument(s) or information included:		
١	11. An Information Disclosure St	atement under 37 C.F.R. 1.97 and 1.98.		
١	12. An Assignment document for	recording. A separate cover sheet in complia	ince with 37	7 CFR 3.28 and 3.31 is included.
I	☐ 13. A First preliminary amendment			
	14. A Second or Subsequent prelin	ninary amendment.		
ı	15. A substitute specification.			
l	☐ 16. A change of power of attorney	and/or address letter.		
l	17. A computer-readable form of the	he sequence listing in accordance with Pe	CT Rule 13	3ter.2 & 35 USC 1.821-825.
	18. A second copy of the published	l international application under 35 USC	154(d)(4).	•
	19. A second copy of the English to	ranslation of the international application	under 35	USC 154(d)(4).
ļ	20. Other items or information:			
١				
		ng Requirements under 35 U.S.C. 371.		
	does not accompany this response, appl	n of time is required to be submitted herewith licant hereby petitions under 37 CFR 1.136(a) ubmission timely. Any fee is authorized in 1) for an exte	
l	months as are required to render this st	admiddion diniery. They for is addionized in f		Date: April 26, 2001

U.S. APPLICATION	NNO (4533 I	NTERNATIONAL A PCT/FR99		ION NO.	A	TTORNEY DOO P07180US00	
X 21. The followin	ng fees are submitted					CALCULATION	NS PTO USE ONLY
X Basic National l	Fee (37 CFR 1.492 (a) (1)-(5):				,*	
Neither Int'l	Prelim. Exam. fee no	Int'l Search fee par	id to USP	ТО	\$1000		!
X Search Repor	t has been prepared b	y the EPO or JPO			\$ 860	,	+
☐ No Int'l Prelim	n. Ex. fee paid to USPTO	O but Int'l Search fee	paid to US	PTO	\$ 710		•
☐ International	preliminary examinat	ion fee paid to USP	PTPO		\$ 690	, ,	
Int'l Prelim. E	x. fee paid to USPTO &	all claims satisfied Po	CT Art. 33	(1)-(4)	\$ 100	٠,	,,,,,
		APPROPRIATE B		EE AMOU	UNT =	\$ 860.00	
	30 for furnishing the c claimed priority date			_	mos. mos. +	\$	
CLAIMS	NUMBER FILED	NUMBER EXTR	RA .	RATE	•		
Total Claims	- 20 =			X \$18	=	\$	
Independent Claims	- 03 =	=	\$				
☐ Multiple Depend	lent Claim(s) (if appli	=	\$				
		ons =	\$ 860.00				
Applicant claims above are reduce	s small entity status. Sed by $\frac{1}{2}$.	See 37 CFR 1.27. Th	he fees ind	dicated	<u>-</u>	\$	
·				SUBTO	TAL =	\$ 860.00	
	\$130 for furnishing the laimed priority date (37)		ater than		mos. mos. +	\$	
			TAL NAT			\$ 860.00	
	the enclosed assignment appropriate cover sheet				e +	\$	
		TOTA	AL FEES	ENCLO	SED =	\$ 860.00	
				Amou	nt to be	Refunded	\$
				mou	<i></i> 10 00	Charged	\$
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i	the amount of \$ 860.0 ge my Deposit Accoun				over the	above fees	
X c. The Commiss	sioner is hereby authorize that No. 12-0555.						
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	propriate time limit u b)) must be filed and p						ive (37 CFR
SEND ALL CORRE	SPONDENCE TO:), (ChI	
B. Aaron S		1	SIGNATU	JRE:/`	vegu	r S. puh	en
At the address (below	v) of CUSTOMER N	IO. 00881.	NAME: D	ouglas E.	Jackson	•	
	& TAYLOR, P	· · · · · · · · · · · · · · · · · · ·	REG. NO.	: 28,518			
SUITE 90	RTH FAIRFAX S 00	P	PHONE N	IO.: 703-7	39-4900)	
1	DRIA, VA 2231	.4	Date: Apri	il 26, 200	1		

PATENT

IN THE UNITED STATES PATENT AND TRADEMARK OFFICE

In re patent application of: AUJAME et al.

Serial No.: 09/830,433

Examiner:

Filed: April 26, 2001

Art Unit:

For: NUCLEIC ACID AND POLYPEPTIDES SPECIFIC

Docket No.: P07180US00/BAS

OF THE NEISSERIA GENUS...

PRELIMINARY AMENDMENT

Honorable Commissioner for Patents

Washington, DC 20231

SIR:

In response to the Notice dated December 6, 2001, please amend the application as follows:

IN THE SPECIFICATION:

After Page 49, please substitute the attached Sequence Listing for any Sequence Listing previously filed in the application.

REMARKS

By this Preliminary Amendment, Applicants are submitting a revised Sequence Listing which overcomes the objections pointed out in the Notice dated December 6, 2001, as well as a copy of the paper sequence in computer readable form.

STATEMENT UNDER 37 CFR § 1.821

Applicants hereby certify in accordance with 37 C.F.R. 1.821(f) that the content of the enclosed paper sequence listing and computer readable form of the sequence listing are the same. In accordance with 37 C.F.R. 1.821(g), Applicants hereby certify that the enclosed submission contains no new matter.

In light of the foregoing, it is submitted that all prior objections have been overcome, and that the present application should be examined and passed on to allowance at the earliest possible time.

Respectfully submitted,

LARSON & TAYLOR, PLC

Date: February 5, 2002

Transpotomac Plaza 1199 N. Fairfax Street Suite 900 Alexandria, VA 22314 (703) 739-4900 B. Aaron Schulman Registration No. 31,877

IN THE UNITED STATES PATENT AND TRADEMARK OFFICE

Patent

In re patent application of: AUJAME et al.

Serial No.: 09/830,433

Examiner:

Filed: April 26, 2001

Art Unit:

For: NUCLEIC ACID AND POLYPEPTIDES SPECIFIC

Docket No.:

OF THE NEISSERIA GENUS...

P07180US00/BAS

PRELIMINARY AMENDMENT

Assistant Commissioner for Patents Washington, D.C.

SIR:

Prior to examination, please amend the above-identified application as follows.

IN THE SPECIFICATION:

After page 49, please insert the enclosed Sequence Listing as a substitute for the one filed in the original application.

IN THE CLAIMS:

A clean version of the amended claims is provided herewith in **Attachment A**. It will be noted that the claims have been amended relative to the previously provided version as shown by the marked up version thereof in **Attachment B** provided herewith.

REMARKS

By this Amendment, the claims have been rewritten to reduce the multiple dependencies. In addition, in response to the Notice to Comply with the sequence listing requirements, a computer readable form and paper copy of the Sequence Listing is now provided, and Applicants state that the paper copy and computer readable form are identical and add no new matter to the application.

Examination and allowance of the present application is thus earnestly solicited.

Respectfully submitted,

Date: 16 August 2001

B. Aaron Schulman Registration No. 31,877

LARSON & TAYLOR PLC Transpotomac Plaza 1199 North Fairfax Street, Suite 900 Alexandria, Virginia 22314 (703) 739-4900

ATTACHMENT A

Clean Replacement/New Claims

Following herewith is a clean copy of each claim which replaces each previous claim having the same number and each new claim.

- 7. (Amended) Expression vector comprising an expression cassette in which a nucleotide sequence as defined in Claim 1 is placed under conditions allowing its expression in a host cell.
 - 9. Canceled.
- 10. (Amended) Monospecific antibody directed against a polypeptide according to Claim 5.
- 11. (Amended) Use of a nucleic acid according to Claim 1, or of a polypeptide specific for pathogenic *Neisseria* strains or of antigenic fragments thereof, for manufacturing a pharmaceutical composition intended for vaccination against *Neisseria*.
- 12. (New) A pharmaceutical composition comprising a nucleic acid according to Claim 1, in naked form or in combination with at least one agent facilitating transfection, and optionally in combination with a pharmaceutically acceptable vehicle.

- 13. (New) A pharmaceutical composition comprising a vaccination vector comprising a nucleotide sequence according to Claim 1, such as in particular a virus or a bacterium, and optionally in combination with a pharmaceutically acceptable vehicle.
- 14. (New) A pharmaceutical composition comprising a polypeptide according to Claim 5, optionally in combination with a pharmaceutically acceptable vehicle.

ATTACHMENT B

Marked Up Replacement Claims

Following herewith is a marked up copy of each rewritten claim.

- 7. (Amended) Expression vector comprising an expression cassette in which a nucleotide sequence as defined in ene of Claims 1 to 4 Claim 1 is placed under conditions allowing its expression in a host cell.
 - 9. Canceled.
- 10. (Amended) Monospecific antibody directed against a polypeptide according to either of Claims 5 and 6 Claim 5.
- 11. (Amended) Use of a nucleic acid according to one of Claims 1 to 4 Claim 1, or of a polypeptide specific for pathogenic *Neisseria* strains or of antigenic fragments thereof, according to either of Claims 5 and 6, for manufacturing a pharmaceutical composition intended for vaccination against *Neisseria*.
- 12. (New) A pharmaceutical composition comprising a nucleic acid according to Claim 1, in naked form or in combination with at least one agent facilitating transfection, and optionally in combination with a pharmaceutically acceptable vehicle.

- 13. (New) A pharmaceutical composition comprising a vaccination vector comprising a nucleotide sequence according to Claim 1, such as in particular a virus or a bacterium, and optionally in combination with a pharmaceutically acceptable vehicle.
- 14. (New) A pharmaceutical composition comprising a polypeptide according to Claim 5, optionally in combination with a pharmaceutically acceptable vehicle.

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Trp Leu Phe Ala Tyr Thr Ser Asp His Gly Gln Tyr Val Arg Gln Asp 425

Ile Tyr Asn Gln Gly Thr Val Gln Pro Asp Ser Tyr Leu Val Pro Leu 440

Val Leu Tyr Ser Ser Asn Lys Ala Val Gln Gln Ala Ala Asn Gln Ala 455

Phe Ala Pro Cys Glu Ile Ala Phe His Gln Gln Leu Ser Thr Phe Leu 470

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Glu Thr Glu Ala Lys Pro Thr Asp Ile Arg His Val Lys Glu Ile Gly 195 200 205

His Ile Asp Val Val Ser His Ile Ile Gly Gly Arg Ser Val Asp Gly

Arg Pro Ala Gly Gly Ile Ala Pro Asp Ala Thr Leu His Ile Met Asn

215

230

210

170

235

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- Lys Ala Met Asn Gly Pro Ala Ser Phe Pro Phe Gly Asp Phe Thr Ala 465 470 475 480
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935

taa

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Gln	Pro	Leu	Ser 980	Asp	Lys	Ala	Val	Leu 985	Phe	Ala	Thr	Ala	Gly 990	Val	Glu	
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aat Asr	tac n Tyr	gaa Glu 275	ı Ala	tto Phe	agt Sei	gaa Glu	a gad 1 Asp 280) Phe	c cto	c ggo ı Gly	c aaa y Lys	a gaa s Glu 28!	ı Arç	c acc	ć gat r Asp	864
acc Th:	c gct r Ala	t ttt a Phe	cat His	cto Lei	c gaa ı Glı	a caq ı Glı	g tto n Phe	e geq	g aat a Ası	t cco	c aad o Asi	c gct n Ala	t act a Thi	c cc r Pro	g ctt o Leu	912

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Asp Pro Thr Ala Pro Leu Phe His Leu Arg Lys Lys Gly Ala Ile Val 55

Pro Lys Glu Glu Tyr Val Glu Ser Phe Asp Asp Leu Gly Lys Thr Arg

Tyr Arg Phe Ile Lys Ser Val Ile Tyr Glu His Met Lys Asn Gly Ala

Ser Leu Val Tyr Asn His Ile Asn Asn Glu Pro Phe Ser Asp His Ile

Ala Arg Gln Val Ala Arg Phe Ala Gly Ala His Thr Ile Val Ser Gly 120

Tyr Leu Ala Phe Gly Ser Asp Glu Ser Tyr Lys Asn His Trp Asp Thr 135 130

Arg Asp Val Tyr Ala Ile Gln Leu Phe Gly Lys Lys Arg Trp Gln Leu 150

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		cag Gln 115														384
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Gln 65		Leu	. Pro	Ala	Ser 70		· Val	Ile	Arg	Val 75		Ala	Pro	Asp	Thr 80	

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Gly Asp Lys Leu Phe Ala Leu Ser Thr Ser Arg Phe Gly Ala Gly Asp 100 110

Ser Val Gln Gln Gln Leu Lys Thr Glu Ala Val Leu Lys Lys Thr Leu 125

135

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Ala Glu Gln Glu Leu Gly Arg Leu Lys Leu Ile His Gly Asn Glu Thr

Ile Ser Gln Gln Ile Asp Gly Gln Lys Arg Arg Ile Arg Leu Ala Glu 165 170 175

Glu Met Leu Gln Lys Tyr Arg Phe Leu Ser Ala Asn Asp Ala Val Pro $180 \hspace{1cm} 185 \hspace{1cm} 190 \hspace{1cm}$

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Asn Leu Thr Leu Ala Ser Leu Pro Lys Arg His Glu Thr Glu Gln Ser
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85 90 95

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				gta Val 165												528
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Tyr Leu Val Lys Ile Lys Pro Asp Lys Pro Thr Ile Thr Ala Tyr Gly
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Ser Met Gln Arg Gln Gln His Ile Asp Ala Glu Leu Leu Thr Asp Ala
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Asn Val Arg Phe Glu Gln Pro Leu Glu Lys Asn Asn Tyr Val Leu Ser
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 Thr Ala Phe Lys Thr Gly Met Cys Leu Gly Ser Asn Asn Leu Ser Arg
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Asn Val Arg Phe Glu Gln Pro Leu Glu Lys Asn Asn Tyr Val Leu Ser

50 55 60

Glu Asp Glu Thr Pro Cys Thr Arg Val Asn Tyr Ile Ser Leu Asp Asp Lys Thr Ala Arg Lys Phe Ser Phe Leu Pro Ser Val Leu Met Lys Glu 90 Thr Ala Phe Lys Thr Gly Met Cys Leu Gly Ser Asn Asn Leu Ser Arg 105 Leu Gln Lys Ala Ala Gln Gln Ile Leu Ile Val Arg Gly Tyr Leu Thr 120 Ser Gln Ala Ile Ile Gln Pro Gln Asn Met Asp Ser Gly Ile Leu Lys 135 Leu Arg Val Ser Ala Gly Glu Ile Arg Asp Ile Arg Tyr Glu Glu Lys 155 Arg Asp Ala Lys Ser Ala Glu Gly Ser Ile Ser Ala Phe Asn Asn Lys 170 Leu Pro Leu Tyr Arg Asn Lys Ile Leu Asn Leu Arg Asp Val Glu Gln Gly Leu Glu Asn Leu Arg Arg Leu Pro Ser Val Lys Thr Asp Ile Gln Ile Ile Pro Ser Glu Glu Glu Gly Lys Ser Asp Leu Gln Ile Lys Trp Gln Gln Asn Lys Pro Ile Arg Phe Ser Ile Gly Ile Asp Asp Ala Gly 235 Gly Lys Thr Thr Gly Lys Tyr Gln Gly Asn Val Ala Leu Ser Ser Asp Asn Pro Leu Gly Leu Ser Asp Ser Phe Tyr Val Ser Tyr Gly Arg Gly 265 Leu Val His Lys Thr Asp Leu Thr Ala Ala Thr Gly Thr Glu Thr Glu 280 Ser Gly Ser Arg Ser Tyr Ser Val His Tyr Ser Val Pro Val Lys 295 Trp Leu Phe Ser Phe Asn His Asn Gly His Arg Tyr His Glu Ala Thr 315 Glu Gly Tyr Ser Val Asn Tyr Asp Tyr Asn Gly Lys Gln Tyr Gln Ser 330 Ser Leu Ala Ala Glu Arg Met Leu Trp Pro Pro Ser Phe Pro Gln Thr 345 Ser Val Arg Met Lys Leu Trp Thr Arg Gln Thr Tyr Lys Tyr Ile Asp 360 Asp Ala Glu Ile Glu Val Gln Arg Arg Ser Ala Gly Trp Glu Ala 370 375 Glu Leu Arg His Arg Ala Tyr Leu His Arg Trp Gln Leu Asp Gly Lys 395

Leu Ser Tyr Lys Arg Gly Thr Gly Met Arg Gln Ser Met Pro Ala Pro

405 Glu Glu Asn Gly Gly Gly Thr Ile Pro Ala Thr Ser Arg Met Lys Ile 425 Ile Thr Ala Gly Leu Asp Ala Ala Pro Ser Met Leu Gly Lys Gln 440 Gln Phe Phe Tyr Ala Thr Ala Ile Gln Ala Gln Trp Asn Lys Thr Pro 455 Leu Val Ala Gln Asp Lys Leu Ser Ile Gly Ser Arg Tyr Thr Val Arg 470 Gly Phe Asp Gly Glu Gln Ser Leu Phe Gly Glu Arg Gly Phe Tyr Trp 485 490 Gln Asn Thr Leu Thr Trp Tyr Phe His Pro Asn His Gln Phe Tyr Leu 505 Gly Ala Asp Tyr Gly Arg Val Ser Gly Glu Ser Ala Gln Tyr Val Ser 520 Gly Lys Gln Leu Met Gly Ala Val Val Gly Phe Arg Gly Gly His Lys 535 Val Gly Gly Met Phe Ala Tyr Asp Leu Phe Ala Gly Lys Pro Leu His 555 Lys Pro Lys Gly Phe Gln Thr Thr Asn Thr Val Tyr Gly Phe Asn Leu 570 Asn Tyr Ser Phe <210> 21 <211> 411 <212> DNA <213> Neisseria meningitidis <220> <221> CDS <222> (1)..(408) <400> 21 atg att gaa ttt gtc cga gcc aaa aaa cgg ctg ctt tgg gca ttt gtg Met Ile Glu Phe Val Arg Ala Lys Lys Arg Leu Leu Trp Ala Phe Val ctt ttg ctt gtg tgg acg tgc ggt tac cga tac gcc gcc gac aag gcc 96 Leu Leu Val Trp Thr Cys Gly Tyr Arg Tyr Ala Ala Asp Lys Ala 25 gaa gcg aaa caa acc gcc ctg att gcc acc tat cgg cat tct tct atg 144 Glu Ala Lys Gln Thr Ala Leu Ile Ala Thr Tyr Arg His Ser Ser Met 40

gtt gcg gcg gaa caa tac gcc ttg cag ctt aaa aaa gcg cag gac gaa Val Ala Ala Glu Gln Tyr Ala Leu Gln Leu Lys Lys Ala Gln Asp Glu

agg cag cgg tgg tac gac ttt tcc caa aaa caa gga aga aag ccc gtg Arg Gln Arg Trp Tyr Asp Phe Ser Gln Lys Gln Gly Arg Lys Pro Val

75

55

70

192

240

aaa aaa cag tat ccg, ccg caa acg aaa aaa gcc ggc tat ctg aaa acc Lys Lys Gln Tyr Pro Pro Gln Thr Lys Lys Ala Gly Tyr Leu Lys Thr 85 90 95	288
aag gaa gaa ctg ctt gcg gaa ttg gct tgc ctt aaa gcg gaa atg gct Lys Glu Glu Leu Leu Ala Glu Leu Ala Cys Leu Lys Ala Glu Met Ala 100 105 110	336
gcc cta aaa aag ctc gat gcc tta atc tat ggg aaa gaa gtg cgg cag Ala Leu Lys Lys Leu Asp Ala Leu Ile Tyr Gly Lys Glu Val Arg Gln 115 120 125	384
aaa gaa cgc aac tcg tcg cag ggt taa Lys Glu Arg Asn Ser Ser Gln Gly 130 135	411
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Val Ala Ala Glu Gln Tyr Ala Leu Gln Leu Lys Lys Ala Gln Asp Glu 50 55 60	
Arg Gln Arg Trp Tyr Asp Phe Ser Gln Lys Gln Gly Arg Lys Pro Val 65 70 75 80	
Lys Lys Gln Tyr Pro Pro Gln Thr Lys Lys Ala Gly Tyr Leu Lys Thr 85 90 95	
Lys Glu Glu Leu Leu Ala Glu Leu Ala Cys Leu Lys Ala Glu Met Ala 100 105 110	
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														cgc Arg		192
	_			_		-		-						ttt Phe	_	240
	-	-	_											ttt Phe 95		288
														gcc Ala		336
														gac Asp		384
														ggc Gly		432
														aac Asn		480
agc Ser	gaa Glu	tac Tyr	gac Asp	cac His 165	ggt Gly	acg Thr	atg Met	ttc Phe	tat Tyr 170	acc Thr	gcc Ala	ccc Pro	aag Lys	gaa Glu 175	ggc Gly	528
														gaa Glu		576
agt Ser	aaa Lys	aaa Lys 195	ttg Leu	cct Pro	ttt Phe	act Thr	gtg Val 200	ttg Leu	acc Thr	gcc Ala	ccc Pro	caa Gln 205	gtt Val	aat Asn	gaa Glu	624
gac Asp	agt Ser 210	gtt Val	gaa Glu	gag Glu	acc Thr	gtc Val 215	cgt Arg	aaa Lys	atc Ile	aaa Lys	gaa Glu 220	acc Thr	gtc Val	ggc Gly	aat Asn	672
atg Met 225	ccc Pro	gtt Val	tac Tyr	ctg Leu	act Thr 230	ttc Phe	gac Asp	ata Ile	gac Asp	tgc Cys 235	ctc Leu	gac Asp	ccg Pro	tcg Ser	ttc Phe 240	720
														gac Asp 255		768
									Asp					ggt Gly		816
gat	gtt	gta	gaa	gtt	gcc	ccc	tct	tac	gac	caa	tcc	gac	att	acc	gct	864

Asp Val Val Glu Val Ala Pro Ser Tyr Asp Gln Ser Asp Ile Thr Ala 275 · · · 280 285	
ttg gcc ggc gcc aca att gcc ttg gaa atg ctt tac ctt caa ggt gcg Leu Ala Gly Ala Thr Ile Ala Leu Glu Met Leu Tyr Leu Gln Gly Ala 290 295 300	912
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Ser Gly Arg Ser Gly Ala Arg Phe Gly Pro Glu Ala Ile Arg Arg Ala 50 55 60	
Ser Val Asn Leu Ala Trp Glu His Arg Arg Phe Pro Trp Thr Phe Asp 65 70 75 80	
Val Arg Glu Arg Leu Asn Ile Ile Asp Cys Gly Asp Leu Val Phe Ser 85 90 95	
Phe Gly Asp Ser Arg Asp Phe Val Glu Lys Met Glu Ala His Ala Gly 100 105 110	
Lys Leu Leu Ser Ser Gly Lys Arg Cys Leu Ser Leu Gly Gly Asp His 115 120 125	
Phe Ile Thr Leu Pro Leu Leu Arg Ala His Ala Arg Tyr Phe Gly Lys 130 135 140	
Leu Ala Leu Ile His Phe Asp Ala His Thr Asp Thr Tyr Asp Asn Gly 145 150 155 160	
Ser Glu Tyr Asp His Gly Thr Met Phe Tyr Thr Ala Pro Lys Glu Gly 165 170 175	
Leu Ile Asp Pro Ser Arg Ser Val Gln Ile Gly Ile Arg Thr Glu His 180 185 190	
Ser Lys Lys Leu Pro Phe Thr Val Leu Thr Ala Pro Gln Val Asn Glu 195 200 205	
Asp Ser Val Glu Glu Thr Val Arg Lys Ile Lys Glu Thr Val Gly Asn 210 215 220	
Met Pro Val Tyr Leu Thr Phe Asp Ile Asp Cys Leu Asp Pro Ser Phe 225 230 235 240	
Ala Pro Gly Thr Gly Thr Pro Val Cys Gly Gly Leu Ser Ser Asp Arg 245 250 255	

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                                                                   96
att ccc tac ccc gtc acc agg cgg att gcc tca agt ttg tat tcg acc
Ile Pro Tyr Pro Val Thr Arg Arg Ile Ala Ser Ser Leu Tyr Ser Thr
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gaa tat ttt gtc gta tgc ttt ctg cgt ttg atg cca ctc tct ccg tgt
Glu Tyr Phe Val Val Cys Phe Leu Arg Leu Met Pro Leu Ser Pro Cys
                              40
aat ctg tat ttt gtc acc cat ctg cgt acc aat gaa tcg gaa ata gaa
                                                                   192
Asn Leu Tyr Phe Val Thr His Leu Arg Thr Asn Glu Ser Glu Ile Glu
     50
                         55
                                                                   240
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Arg Trp Ser Ala Val Pro Cys Gln Ile Val Leu Asn Asp Gly Lys Ser
                                          75
                                                                   288
gaa ttc ggc gga ttc gca ttt gaa gtg caa ctt tcc cta aca gaa aaa
Glu Phe Gly Gly Phe Ala Phe Glu Val Gln Leu Ser Leu Thr Glu Lys
                 85
                                      90
                                                                   336
ggc cag tat gcg gta gca tac gac ctt tcc tgc aag aaa gat tgc cat
Gly Gln Tyr Ala Val Ala Tyr Asp Leu Ser Cys Lys Lys Asp Cys His
            100
                                 105
                                                                   384
qaq cta cac qca act gac cca agg cga acg ata cca cat cca ata cct
Glu Leu His Ala Thr Asp Pro Arg Arg Thr Ile Pro His Pro Ile Pro
        115
                             120
                                                                   426
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Val Pro Pro Leu His Arg His Arg Asn Arg Gln Thr Ala
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Arg Trp Ser Ala Val Pro Cys Gln Ile Val Leu Asn Asp Gly Lys Ser
Glu Phe Gly Gly Phe Ala Phe Glu Val Gln Leu Ser Leu Thr Glu Lys
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Gly Gln Tyr Ala Val Ala Tyr Asp Leu Ser Cys Lys Lys Asp Cys His
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Glu Leu His Ala Thr Asp Pro Arg Arg Thr Ile Pro His Pro Ile Pro
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Gly Ile Met Leu Leu Lys Val Val Pro Glu Arg Thr Val Ser Ala Asp
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                                  25
gca aaa acc aga gac ccg atg tgg gac aat gcg gct tta cag acc agc
Ala Lys Thr Arg Asp Pro Met Trp Asp Asn Ala Ala Leu Gln Thr Ser
                              40
gaa ggc gta aat ttt att gct cgt ttc cta gga ttt ttt agc gat ggg
                                                                   192
Glu Gly Val Asn Phe Ile Ala Arg Phe Leu Gly Phe Phe Ser Asp Gly
     50
                          55
                                                                    240
qaa tac cgc tat gtg gat gtc ctg caa ccc aac cat tcc gat att att
Glu Tyr Arg Tyr Val Asp Val Leu Gln Pro Asn His Ser Asp Ile Ile
 65
                      70
                                          75
cgg tat tca ggt aaa gat ttt ccg cta aat caa ata ctt aac cat ata
Arg Tyr Ser Gly Lys Asp Phe Pro Leu Asn Gln Ile Leu Asn His Ile
                  8.5
                                      90
cac ccc gcc cgt tat gcg gta acg ttc gaa aac aat gtc gat tcc aag
His Pro Ala Arg Tyr Ala Val Thr Phe Glu Asn Asn Val Asp Ser Lys
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Met Glu Gln Ser·Gly, Lys Phe Ser Trp Ser Ala Ala Ala Phe Trp Asp

240

ctg cgc agg cac tga

Leu Arg Arg His

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	Gly	Ile	Met	Leu 20	Leu	Lys	Val	Val	Pro 25	Glu	Arg	Thr	Val	Ser 30	Ala	Asp	
	Ala	Lys	Thr 35	Arg	Asp	Pro	Met	Trp	Asp	Asn	Ala	Ala	Leu 45	Gln	Thr	Ser	
	Glu	Gly 50	Val	Asn	Phe	Ile	Ala 55	Arg	Phe	Leu	Gly	Phe 60	Phe	Ser	Asp	Gly	
	Glu 65		Arg	Tyr	Val	Asp 70	Val	Leu	Gln	Pro	Asn 75	His	Ser	Asp	Ile	Ile 80	
The state of the s	Arg	Tyr	Ser	Gly	Lys 85	Asp	Phe	Pro	Leu	Asn 90	Gln	Ile	Leu	Asn	His 95	Ile	
	His	Pro	Ala	Arg 100	Tyr	Ala	Val	Thr	Phe 105	Glu	Asn	Asn	Val	Asp 110	Ser	Lys	
	Leu	. Arg	Arg 115	His													
The fact has been the first that the	<21 <21	0> 2 1> 1 2> D 3> N	404	eria	men	ingi [.]	tidi	S									
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	tgo Cys	c ctg s Leu	aca Thr	ctg Leu 20	Thr	ccc Pro	tat Tyr	ttg Leu	caa Gln 25	His	gaa Glu	cta Leu	ttt Phe	tcg Ser 30	gct Ala	atg Met	96
	aaa Lys	a tcc S Ser	tat Tyr 35	Phe	tcc Ser	aaa Lys	tat Tyr	atc Ile 40	Leu	ccc Pro	gtt Val	tca Ser	ctt Leu 45	ttt Phe	acc Thr	ttg Leu	144
	cca Pro	a cta	tcc Ser	ctt Leu	tcc Ser	cca Pro	tcc Ser	gtt Val	tcg Ser	gct	ttt. Phe	acg Thr	ctg Leu	cct Pro	gaa Glu	gca Ala	192

55

tgg cgg gcg gcg cag caa cat tcg gct gat ttt caa gcg tcc cat tac

105

Trp 65	Arg	Ala	Ala		Gln 70	His	Ser	Ala	Asp	Phe 75	Gln	Ala	Ser	His	Tyr 80	
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														cca Pro		336
att Ile	tct Ser	tcc Ser 115	acc Thr	cgc Arg	gaa Glu	aca Thr	cag Gln 120	gga Gly	tgg Trp	agc Ser	gtg Val	cag Gln 125	gtg Val	gga Gly	caa Gln	384
acc Thr	tta Leu 130	ttt Phe	gac Asp	gct Ala	gcc Ala	aaa Lys 135	ttt Phe	gca Ala	caa Gln	tac Tyr	cgc Arg 140	caa Gln	agc Ser	agg Arg	ttc Phe	432
gat Asp 145	acg Thr	cag Gln	gct Ala	gca Ala	gaa Glu 150	cag Gln	cgt Arg	ttc Phe	gat Asp	gcg Ala 155	gca Ala	cgc Arg	gaa Glu	gaa Glu	ttg Leu 160	480
ctg Leu	ttg Leu	aaa Lys	gtt Val	gcc Ala 165	gaa Glu	agt Ser	tat Tyr	ttc Phe	aac Asn 170	gtt Val	tta Leu	ctc Leu	agc Ser	cga Arg 175	gac Asp	528
acc Thr	gtt Val	gcc Ala	gcc Ala 180	cat His	gcg Ala	gcg Ala	gaa Glu	aaa Lys 185	gag Glu	gct Ala	tat Tyr	gcc Ala	cag Gln 190	cag Gln	gta Val	576
agg Arg	cag Gln	gcg Ala 195	cag Gln	gct Ala	tta Leu	ttc Phe	aat Asn 200	aaa Lys	ggt Gly	gct Ala	gcc Ala	acc Thr 205	gcg Ala	ctg Leu	gat Asp	624
att Ile	cac His 210	gaa Glu	gcc Ala	aaa Lys	gcc Ala	ggt Gly 215	tac Tyr	gac Asp	aat Asn	gcc Ala	ctg Leu 220	gcc Ala	caa Gln	gaa Glu	atc Ile	672
gcc Ala 225	gta Val	ttg Leu	gct Ala	gag Glu	aaa Lys 230	caa Gln	acc Thr	tat Tyr	gaa Glu	aac Asn 235	cag Gln	ttg Leu	aac Asn	gac Asp	tac Tyr 240	720
acc Thr	gac Asp	ctg Leu	gat Asp	agc Ser 245	aaa Lys	caa Gln	atc Ile	gag Glu	gcc Ala 250	ata Ile	gat Asp	acc Thr	gcc Ala	aac Asn 255	ctg Leu	768
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cag Gln	cgc Arg	att Ile 275	gcc Ala	tta Leu	tcc Ser	aac Asn	aat Asn 280	cat His	gaa Glu	tac Tyr	cgg Arg	atg Met 285	cag Gln	cag Gln	ctt Leu	864
gcc Ala	ctg Leu 290	Gln	agc Ser	agc Ser	gga Gly	cag Gln 295	gcg Ala	ctt Leu	cgg Arg	gca Ala	gca Ala 300	cag Gln	aac Asn	agc Ser	cgc Arg	912
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tca Ser	tct Ser	gcg Ala	cag Gln	aat Asn 325	Asn	gac Asp	tac Tyr	cac His	tat Tyr 330	Arg	ggg Gly	aaa Lys	ggg Gly	atg Met 335	Ser	1008

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acc Thr 385	gaa Glu	agc Ser	ggt Gly	gcg Ala	gcg Ala 390	cgt Arg	tac Tyr	caa Gln	atc Ile	atg Met 395	gcg Ala	caa Gln	gaa Glu	cgg Arg	gtt Val 400	1200
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gcc Ala	caa Gln	gca Ala 435	gaa Glu	cag Gln	aaa Lys	ctg Leu	gct Ala 440	caa Gln	gca Ala	cgg Arg	tat Tyr	aaa Lys 445	ttc Phe	atg Met	ctg Leu	1344
gct Ala	tat Tyr 450	ttg Leu	cgc Arg	ttg Leu	gtg Val	aaa Lys 455	gag Glu	agc Ser	ggg Gly	tta Leu	ggg Gly 460	ttg Leu	gaa Glu	acg Thr	gta Val	1392
+++	gcg	gaa	taa													1404
	Ala	Glu														
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115 120 125

Thr Leu Phe Asp Ala Ala Lys Phe Ala Gln Tyr Arg Gln Ser Arg Phe 130 135 140

Leu Leu Lys Val Ala Glu Ser Tyr Phe Asn Val Leu Leu Ser Arg Asp 165 170 175

Thr Val Ala Ala His Ala Ala Glu Lys Glu Ala Tyr Ala Gln Gln Val 180 185 190

Arg Gln Ala Gln Ala Leu Phe Asn Lys Gly Ala Ala Thr Ala Leu Asp 195 200 205

Ile His Glu Ala Lys Ala Gly Tyr Asp Asn Ala Leu Ala Gln Glu Ile 210 215 220

Ala Val Leu Ala Glu Lys Gln Thr Tyr Glu Asn Gln Leu Asn Asp Tyr 225 230 235 240

Thr Asp Leu Asp Ser Lys Gln Ile Glu Ala Ile Asp Thr Ala Asn Leu 245 250 255

Leu Ala Arg Tyr Leu Pro Lys Leu Glu Arg Tyr Ser Leu Asp Glu Trp 260 265 270

Gln Arg Ile Ala Leu Ser Asn Asn His Glu Tyr Arg Met Gln Gln Leu 275 280 285

Ala Leu Gln Ser Ser Gly Gln Ala Leu Arg Ala Ala Gln Asn Ser Arg 290 295 300

Tyr Pro Thr Val Ser Ala His Val Gly Tyr Gln Asn Asn Leu Tyr Thr 305 310 315 320

Ser Ser Ala Gln Asn Asn Asp Tyr His Tyr Arg Gly Lys Gly Met Ser 325 330 335

Val Gly Val Gln Leu Asn Leu Pro Leu Tyr Thr Gly Gly Glu Leu Ser $340 \hspace{1.5cm} 345 \hspace{1.5cm} 350 \hspace{1.5cm}$

Gly Lys Ile His Glu Ala Glu Ala Gln Tyr Gly Ala Ala Glu Ala Gln 355 360 365

Leu Thr Ala Thr Glu Arg His Ile Lys Leu Ala Val Arg Gln Ala Tyr 370 375 380

Thr Glu Ser Gly Ala Ala Arg Tyr Gln Ile Met Ala Gln Glu Arg Val 385 390 395 400

Leu Glu Ser Ser Arg Leu Lys Leu Lys Ser Thr Glu Thr Gly Gln Gln 405 410 415

Tyr Gly Ile Arg Asn Arg Leu Glu Val Ile Arg Ala Arg Gln Glu Val 420 425 430

Ala Gln Ala Glu Gln Lys Leu Ala Gln Ala Arg Tyr Lys Phe Met Leu 435 440 445

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Phe Ala Glu

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Phe Pro Arg Val Ser Ser Val Val Leu Leu Ile Tyr Val Gly Thr Thr

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Val Gly Asn Leu Pro Gly Ser Leu Tyr Phe Val Gln Ala Leu Phe Phe

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Asp Lys Asp Leu Arg Glu Pro Asp Ala Gly Leu Leu Asn Ile Phe 185

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cgg cgg ttt Arg Arg Phe 145	cag tat ca Gln Tyr Gl 15	n Thr Glu	aaa ata Lys Ile	tcc tgc Ser Cys 155	tat gtt Tyr Val	tcc Ser	acc 480 Thr 160
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gaa aat aaa Glu Asn Lys	gaa agc to Glu Ser Tr 180	g tot ttg p Ser Leu	g gtt tac 1 Val Tyr 185	ttt tcc Phe Ser	gac cac Asp His	Gly	ttg 576 Leu
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	aac Asn														
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Ile	Ala	Gln	Thr	Asp 165	Lys	Phe	Leu	Glu	Asp 170		Val	Lys	Ile	Leu 175	Asn
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Met	His	Val 195	Gly	Lys	Gly	Gly	Glu 200		Thr	Leu	Thr	His 205		Ala	Trp
_	_		_		~ 3			-	77 - 3	т	T 1 -	C		70.00	7 00

Lys Arg Gln Ser Tyr Gly Val Pro Leu Val Lys Ile Ser Ser Asp Asp 210 215 220

Thr Arg Arg Glu Met Ile Lys Val Arg Arg Ser Ala Phe Asn Phe Leu

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11 gins 21 gins 11 gins
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Arg Gly Phe Gly Ser Trp Thr Gly Ile Glu Thr Asp Glu Leu Pro Asp Asp Gly Tyr Asp Phe Trp Gly Asn Val Pro Asp Val Gln Gly Glu Gly Asn Asn Leu Ala Phe Ile Asp Gly Leu Pro Asp Asp Pro Ala Pro Trp Tyr Ala Gly Lys Gly Lys Ser Thr Lys Asn Thr Ser Lys Lys 295 <210> 35 <211> 864 <212> DNA <213> Neisseria meningitidis <220> <221> CDS <222> (1)..(861) <400> 35 48 atg atg agt caa cac tct gcc gga gca cgt ttc cgc caa gcc gtg aaa Met Met Ser Gln His Ser Ala Gly Ala Arg Phe Arg Gln Ala Val Lys 96 gaa tog aat cog ott goo gto goo ggt tgo gto aat got tat ttt goa Glu Ser Asn Pro Leu Ala Val Ala Gly Cys Val Asn Ala Tyr Phe Ala cga ttg gcc acc caa agc ggt ttc aaa gcc atc tat ctg tcc ggc ggc Arg Leu Ala Thr Gln Ser Gly Phe Lys Ala Ile Tyr Leu Ser Gly Gly ggc gtg gca gcc tgt tct tgc ggt atc cct gat ttg ggc att acc aca 192 Gly Val Ala Ala Cys Ser Cys Gly Ile Pro Asp Leu Gly Ile Thr Thr 50 atq qaa qat qtq ctq atc qac qca cqc att acq qac aac gtg gat 240 Met Glu Asp Val Leu Ile Asp Ala Arg Arg Ile Thr Asp Asn Val Asp 75 65 acg cct ctg ctg gtg gac atc gat gtg ggt tgg ggc ggt gca ttc aat 288 Thr Pro Leu Leu Val Asp Ile Asp Val Gly Trp Gly Gly Ala Phe Asn 85 att qcc cqt acc att cqc aac ttt qaa cqc qcc qqt qtt gca gcg gtt 336 Ile Ala Arg Thr Ile Arg Asn Phe Glu Arg Ala Gly Val Ala Ala Val 105 384 cac atc gaa gat cag gta gcg caa aaa cgc tgc ggc cac cgt ccg aac His Ile Glu Asp Gln Val Ala Gln Lys Arg Cys Gly His Arg Pro Asn 115 120 aaa gcc att gta tct aaa gat gaa atg gtc gac cgt atc aaa gct gcc 432 Lys Ala Ile Val Ser Lys Asp Glu Met Val Asp Arg Ile Lys Ala Ala 135 130 gta gat gcg cgc gtt gat gag aac ttc gtg att atg gcg cgt acc gat Val Asp Ala Arg Val Asp Glu Asn Phe Val Ile Met Ala Arg Thr Asp

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Met Asp Val Met Arg Thr Gly Val Ser Met Leu Gly Cys Val His Pro 145 150 155 160

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Gly His Phe Leu His Leu Leu His Gly Lys Arg Pro Ser Glu Ser His 210 215 220

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	tta Leu	ctg Leu	atg Met	gga Gly 20	ata Ile	ttc Phe	ttg Leu	gca Ala	gtt Val 25	tct Ser	gcg Ala	gcc Ala	ctt Leu	ctg Leu 30	aat Asn	gca Ala	96
	acc Thr	atc Ile	ggc Gly 35	ata Ile	ttc Phe	agc Ser	aag Lys	ata Ile 40	ttg Leu	atg Met	gag Glu	cag Gln	ggc Gly 45	ttg Leu	tct Ser	gtt Val	144
	cag Gln	cat His 50	att Ile	gca Ala	ttt Phe	ttg Leu	aaa Lys 55	act Thr	ttg Leu	aca Thr	ggt Gly	ttc Phe 60	gtg Val	ttt Phe	atc Ile	agc Ser	192
	att Ile 65	ttg Leu	ctt Leu	tgc Cys	cgt Arg	acc Thr 70	ggt Gly	ttt Phe	acc Thr	aga Arg	cag Gln 75	att Ile	gcg Ala	gat Asp	att Ile	tca Ser 80	240
	aga Arg	aag Lys	aaa Lys	gag Glu	gca Ala 85	att Ile	ttg Leu	ccg Pro	ttg Leu	ctg Leu 90	tta Leu	aaa Lys	gta Val	gca Ala	att Ile 95	tgt Cys	288
	gct Ala	ttt Phe	ttc Phe	gga Gly 100	att Ile	tat Tyr	acg Thr	ttg Leu	ttt Phe 105	ttc Phe	ttt Phe	gaa Glu	acc Thr	aca Thr 110	gct Ala	tat Tyr	336
	caa Gln	tat Tyr	ggc Gly 115	aat Asn	gct Ala	gcg Ala	aat Asn	gta Val 120	gta Val	gtt Val	gta Val	tta Leu	atg Met 125	gca Ala	tcg Ser	gct Ala	384
	gcc Ala	gta Val 130	tct Ser	gcc Ala	ttg Leu	ata Ile	ttg Leu 135	gac Asp	agc Ser	ata Ile	ctg Leu	tta Leu 140	gat Asp	gaa Glu	cgt Arg	att Ile	432
	tgc Cys 145	att Ile	tct Ser	tca Ser	gtc Val	gtc Val 150	ggt Gly	gtg Val	ggt Gly	ttg Leu	gca Ala 155	gta Val	ttg Leu	Gly	atc Ile	gca Ala 160	480
,	Met	Ile	Ser	Trp	Thr 165	Gly	Glu	Gly	agt Ser	Leu 170	Gly	Leu	Ile	Leu	Asn 175	Ala	528
	Ala	Leu	Ala	Gly 180	Ser	Gly	Tyr	Gly	Cys 185	Phe	Ser	Val	Leu	Ile 190	Lys	,	576
	ttc Phe	ggc	cta Leu 195	Asn	ggc	ggt Gly	att Ile	tat Tyr 200	ttg Leu	aca Thr	cgg Arg	ata Ile	ttg Leu 205	Met	ttt Phe	ttt Phe	624
	gga Gly	agt Ser 210	: Ile	ttt Phe	ttg Leu	ttt Phe	ato Ile 215	Pro	tca Ser	ttg Leu	gaa Glu	ggt Gly 220	Ile	gag Glu	gat Asp	ata Ile	672
	cat His 225	Trp	g caa Glr	ı tgç ı Trp	tct Ser	ttt Phe 230	: Ile	ccç Pro	g cca Pro	cto Leu	ttg Lev 235	ı Ala	ttg Leu	tct Ser	tta Leu	ttg Leu 240	720
	ccg Pro	g aco	g att	t tta e Lei	a gga a Gly 245	y Phe	tat Tyr	tgt Cys	aca Thr	act Thr 250	: Lys	gca Ala	ttç Lev	gat 1 Asp	tat Tyr 255	ttg Leu	768
	agt Ser	gct Ala	gcq a Ala	g aaq a Lys	g gta s Val	a caq l Glr	g gta n Val	a act L Thi	gaa c Glu	tto Lei	g gcd ı Ala	c gaç a Glu	g cca n Pro	tto Lev	g ttt ı Phe	gct Ala	816

260 265 270

gcc gta ctg gct tgg ttg ttt ttg aat gaa ata ccg gaa gga cgc ttc

gcc gta ctg gct tgg ttg ttt ttg aat gaa ata ccg gaa gga cgc ttc

Ala Val Leu Ala Trp Leu Phe Leu Asn Glu Ile Pro Glu Gly Arg Phe

275

280

285

ttt gtc ggc gcc att ctg att att gcc ggt att gtg tct atc aat ggg 912
Phe Val Gly Ala Ile Leu Ile Ile Ala Gly Ile Val Ser Ile Asn Gly
290 295 300

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<213> Neisseria meningitidis

<400> 40

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Thr Ile Gly Ile Phe Ser Lys Ile Leu Met Glu Gln Gly Leu Ser Val

Gln His Ile Ala Phe Leu Lys Thr Leu Thr Gly Phe Val Phe Ile Ser 50 55 60

Ile Leu Leu Cys Arg Thr Gly Phe Thr Arg Gln Ile Ala Asp Ile Ser 65 70 75 80

Arg Lys Lys Glu Ala Ile Leu Pro Leu Leu Leu Lys Val Ala Ile Cys 85 90 95

Ala Phe Phe Gly Ile Tyr Thr Leu Phe Phe Phe Glu Thr Thr Ala Tyr 100 105 110

Gln Tyr Gly Asn Ala Ala Asn Val Val Val Leu Met Ala Ser Ala 115 120 125

Ala Val Ser Ala Leu Ile Leu Asp Ser Ile Leu Leu Asp Glu Arg Ile 130 135 140

Cys Ile Ser Ser Val Val Gly Val Gly Leu Ala Val Leu Gly Ile Ala 145 150 155 160

Met Ile Ser Trp Thr Gly Glu Gly Ser Leu Gly Leu Ile Leu Asn Ala 165 170 175

Ala Leu Ala Gly Ser Gly Tyr Gly Cys Phe Ser Val Leu Ile Lys Lys 180 185 190

Phe Gly Leu Asn Gly Gly Ile Tyr Leu Thr Arg Ile Leu Met Phe Phe 195 200 205

Gly Ser Ile Phe Leu Phe Ile Pro Ser Leu Glu Gly Ile Glu Asp Ile

His Trp Gln Trp Ser Phe Ile Pro Pro Leu Leu Ala Leu Ser Leu Leu 225 230 235 240

	Ser	Ala	Ala	Lys 260	Val	Gln	Val	Thr	Glu 265	Leu	Ala	Glu	Pro	Leu 270	Phe	Ala	
	Ala	Val	Leu 275	Ala	Trp	Leu	Phe	Leu 280	Asn	Glu	Ile	Pro	Glu 285	Gly	Arg	Phe	
	Phe	Val 290	Gly	Ala	Ile	Leu	Ile 295	Ile	Ala	Gly	Ile	Val 300	Ser	Ile	Asn	Gly	
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٠		1> C		(260	7)				•								
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	gaa Glu	tac Tyr	tac Tyr	gac Asp 20	Ala	cgt Arg	gcg Ala	gcg Ala	tgt Cys 25	gag Glu	gac Asp	atc Ile	aag Lys	ccc Pro 30	ggc Gly	tct Ser	96
	tac Tyr	gac Asp	aag Lys 35	Leu	cct Pro	tac Tyr	acg Thr	agc Ser 40	cgc Arg	att Ile	ttg Leu	gcg Ala	gag Glu 45	aat Asn	ttg Leu	gtc Val	144
	aac Asn	cgc Arg 50	Ala	gac Asp	aaa Lys	gtc Val	gat Asp 55	ttg Leu	ccg Pro	acg Thr	ctg Leu	caa Gln 60	agc Ser	tgg Trp	ctg Leu	ggt Gly	192
	cag Gln 65	Leu	att Ile	gag Glu	gga Gly	aaa Lys 70	cag Gln	gaa Glu	atc Ile	gac Asp	ttt Phe 75	cct Pro	tgg Trp	tat Tyr	ccg Pro	gcg Ala 80	240
	cgg Arg	gtg Val	gto Val	g tgo Cys	cac His 85	Asp	att Ile	ctg Leu	Gly	cag Gln 90	Thr	gcg Ala	ttg Leu	gtg Val	gat Asp 95	ttg Leu	288
	gca Ala	ı ggt ı Gly	cto Lei	g cgc ı Arç 100	, Asp	gcg Ala	att	gcc Ala	gaa Glu 105	ı Lys	ggc	ggc	gat Asp	cct Pro 110	Ala	aaa Lys	336
	gto Val	g aat Asr	ccq Pro	o Val	g gtt L Val	gca Ala	aaa Lys	. ccc Pro 120	Sei	tto Phe	ato Ile	gto Val	gac Asp 125	His	tct Ser	ctg Leu	384
,	gco Ala	gtt a Val	L Glı	a tgo u Cys	c ggc	ggc Gly	tac Tyr 135	: Asp	c cco	c gat o Asp	gcc Ala	tto Phe 140	e Arg	aaa Lys	aac Asr	c cgc n Arg	432
	caa Gli 14!	n Ile	c ga e Gl	a gad u Asj	c aga p Arq	a cgt g Arg 150	g Asr	gaa Glu	a gad ı Ası	c cgt p Arq	tto Phe 155	e His	c tto s Phe	ato E Ile	aac Asr	tgg Trp 160	480

Pro Thr Ile Leu Gly Phe Tyr Cys Thr Thr Lys Ala Leu Asp Tyr Leu . •245, • 250 255

aca aa Thr Ly	ia acc rs Thi	gça. Ala	ttt, Phe 165	gaa Glu	aat Asn	gtg Val	gac Asp	gtg Val 170	att Ile	ccg Pro	gcg Ala	Gly	aac Asn 175	ggc Gly	528
atc at Ile Me	g cad	c caa Gln 180	atc Ile	aat Asn	cta Leu	gaa Glu	aaa Lys 185	atg Met	tcg Ser	ccc Pro	Val	gtc Val 190	caa Gln	gtc Val	576
aaa aa Lys As	ac ggo sn Gly 195	y Val	gcg Ala	ttc Phe	ccc Pro	gat Asp 200	acc Thr	tgc Cys	gtc Val	ggc Gly	acg Thr 205	gat Asp	tcg Ser	cac His	624
acg co Thr Pr 21	co His	c gtc s Val	gat Asp	gcg Ala	ctg Leu 215	ggc Gly	gtg Val	att Ile	tcc Ser	gtg Val 220	ggc Gly	gtg Val	ggc Gly	gga Gly	672
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ccc ga Pro As	at at sp Il	t gtc e Val	ggc Gly 245	gtt Val	gag Glu	ctg Leu	aac Asn	ggc Gly 250	aaa Lys	cgg Arg	cag Gln	gcg Ala	ggc Gly 255	att Ile	768
acg go Thr A	cg ac la Th	g gat r Asp 260	att Ile	gtg Val	ttg Leu	gca Ala	ctg Leu 265	acc Thr	gag Glu	ttt Phe	ctg Leu	cgc Arg 270	aaa Lys	gaa Glu	816
cgc g	tg gt al Va 27	l Gly	gcg Ala	ttt Phe	gtc Val	gaa Glu 280	ttc Phe	ttc Phe	ggc Gly	gag Glu	ggc Gly 285	gcg Ala	aga Arg	agc Ser	864
ctg to Leu S	ct at er Il 90	c ggc e Gly	gac Asp	cgc Arg	gcg Ala 295	acc Thr	att Ile	tcc Ser	aac Asn	atg Met 300	acg Thr	ccg Pro	gag Glu	ttc Phe	912
ggc g Gly A 305	cg ac la Th	t gcc r Ala	gcg Ala	atg Met 310	ttc Phe	gct Ala	att Ile	gat Asp	gag Glu 315	caa Gln	acc Thr	att Ile	gat Asp	tat Tyr 320	960
ttg a Leu L	aa ct ys Le	g acc u Thr	gga Gly 325	cgc Arg	gac Asp	gac Asp	gcg Ala	cag Gln 330	gtg Val	aaa Lys	ttg Leu	gtg Val	gaa Glu 335	Thr	1008
tac g Tyr A	ıcc aa ıla Ly	a acc s Thr 340	Ala	ggc Gly	tta Leu	tgg Trp	gca Ala 345	Asp	gcc Ala	ttg Leu	aaa Lys	acc Thr 350	Ala	gtt Val	1056
tat c Tyr F	cg cg Pro Ai	g Val	ttg L Leu	aaa Lys	ttt Phe	gat Asp 360	Leu	ago Ser	ago Ser	gta Val	acg Thr 365	Arg	aat Asn	atg Met	1104
Ala G	ggc co Sly Pi 370	eg ago co Sei	c aac r Asn	ccg Pro	cac His	: Ala	g cgt Arç	ttt JPhe	gcg Ala	g acc Thr 380	: Ala	gat Asp	ttg Lev	gcc Ala	1152
agc a Ser I 385	aaa go Lys G	gc tto ly Le	g gct u Ala	aaa Lys 390	Pro	tac Tyr	gaa Glu	a gaç ı Glu	cct Pro 395	Ser	a gac Asp	ggc Gl	c caa 7 Glr	a atg n Met 400	1200
ccc q Pro <i>l</i>	gac g Asp G	gc gc ly Al	g gto a Val 405	L Ile	ato Ile	gco Ala	c gcg a Ala	g att a Ile 410	Thi	c agt r Sei	t tgo r Cys	aco Thi	c aad c Asr 415	1 Thr	1248
tcc a	aac c	cg cg	c aad	c gtt	gtt:	gc.	c gc	c gc	g ct	c tto	g gc	g cg	c aad	c gcc	1296

Ser	Asn	Pro	Arg 420.	Asn	Val	Val		Ala 425	Ala	Leu	Leu		Arg 430	Asn	Ala	
aac Asn	tgc Cys	ttc Phe 435	ggg Gly	ctg Leu	aaa Lys	cgc Arg	aaa Lys 440	ccg Pro	tgg Trp	gtc Val	aaa Lys	acc Thr 445	tcg Ser	ttt Phe	gcc Ala	1344
ccc Pro	ggt Gly 450	tcg Ser	aaa Lys	gtg Val	gcg Ala	gaa Glu 455	att Ile	tat Tyr	ttg Leu	aaa Lys	gaa Glu 460	gca Ala	ggc Gly	ctg Leu	ctg Leu	1392
ccc Pro 465	gaa Glu	atg Met	gaa Glu	aaa Lys	ctc Leu 470	ggc Gly	ttc Phe	ggt Gly	atc Ile	gtc Val 475	gcc Ala	ttc Phe	gcc Ala	tgc Cys	acc Thr 480	1440
acc Thr	tgc Cys	aac Asn	ggc Gly	atg Met 485	agt Ser	ggc Gly	gcg Ala	ctg Leu	gat Asp 490	ccg Pro	aaa Lys	atc Ile	cag Gln	aaa Lys 495	gaa Glu	1488
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aac Asn	ttc Phe	gac Asp 515	ggc Gly	cgt Arg	gtc Val	cat His	ccg Pro 520	tat Tyr	gcg Ala	aaa Lys	cag Gln	gct Ala 525	ttc Phe	ctc Leu	gct Ala	1584
tcg Ser	cct Pro 530	ccg Pro	ttg Leu	gtc Val	gtt Val	gcc Ala 535	tac Tyr	gcg Ala	ctg Leu	gca Ala	ggc Gly 540	agt Ser	atc Ile	cgt Arg	ttc Phe	1632
gat Asp 545	Ile	gaa Glu	aac Asn	gac Asp	gta Val 550	ctc Leu	ggc Gly	gtt Val	gca Ala	gac Asp 555	ggc Gly	aag Lys	gaa Glu	atc Ile	cgc Arg 560	1680
ctg Leu	aaa Lys	gac Asp	att Ile	tgg Trp 565	cct Pro	gcc Ala	gat Asp	gaa Glu	gaa Glu 570	atc Ile	gat Asp	gcc Ala	gtc Val	gtt Val 575	gcc Ala	1728
gaa Glu	tat Tyr	gtg Val	aaa Lys 580	ccg Pro	Gln	Gln	ttc Phe	Ara	asp	Val	Tyr	Val	ccg Pro 590	Met	ttc Phe	1776
gac Asp	acc Thr	ggc Gly 595	Thr	gcg Ala	caa Gln	aaa Lys	gca Ala 600	cct Pro	agt Ser	ccg Pro	ctg Leu	tac Tyr 605	Asp	tgg Trp	cgt Arg	1824
Pro	atg Met 610	Ser	acc Thr	tac Tyr	atc Ile	cgc Arg 615	Arg	ccg Pro	cct Pro	tac Tyr	tgg Trp 620	Glu	ggc Gly	gcg Ala	ctg Leu	1872
gca Ala 625	a Gly	g gaa 7 Glu	a cgo ı Arç	aca J Thr	tta Leu 630	Arg	ggt Gly	ato Met	g cgt : Arg	ccq Pro 635) Let	g gcg n Ala	att Ile	ttg Lev	ccc Pro 640	1920
gac Asr	c aac o Asr	ato n Ile	c aco	c acc Thr 645	: Asp	cac His	cto Lev	tco Ser	g ccg Pro 650	Sei	c aat c Asr	gcg Ala	g att	tto E Lev 655	g gcc 1 Ala 5	1968
gto Vai	c agt l Sei	z geo r Ala	c gca a Ala 660	a Gly	gaq Glu	g tat ı Tyı	t ttg Lei	g gcg 1 Ala 665	a Lys	a ato	g ggt t Gly	t ttg y Lei	g cct i Pro 670) GII	a gaa ı Glu	2016
ga Asj	c tto p Pho	c aa e As: 67	n Se	t tad r Tyl	c gca r Ala	a aco	c cad c His 680	s Ar	g Gly	c ga y As _l	c cao	c tto s Let 685	ג Th:	c gco r Ala	c caa a Gln	2064

cgc gct Arg Ala 690	a Thr														2112
gaa gad Glu Asr 705		_		_			_		_	_	-	-		_	2160
ggc gaa Gly Gli															2208
aaa caq Lys Glr															2256
agc cgc Ser Arc															2304
att gtt Ile Val 770	Āla	_				-			_						2352
atg ggd Met Gly 785		_	_	_	_				_			_			2400
ctg caa Leu Glr	_	_		_	-			-		-		_	-		2448
ccg cgo Pro Aro															2496
gtc gaa Val Glu	_		_		_	_		_		-	-		_	_	2544
gta tat Val Ty: 850	Glu														2592
gaa ggg Glu Gly 865	-		-	tag											2610
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Tyr As	p Lys 35	Leu	Pro	Tyr	Thr	Ser 40	Arg	Ile	Leu	Ala	Glu 45	Asn	Leu	Val	
Asn Ar	g Ala	Asp	Lys	Val	Asp	Leu	Pro	Thr	Leu	Gln	Ser	Trp	Leu	Gly	

50 55 60

Gln Leu Ile Glu Gly Lys Gln Glu Ile Asp Phe Pro Trp Tyr Pro Ala
65 70 75 80

Arg Val Val Cys His Asp Ile Leu Gly Gln Thr Ala Leu Val Asp Leu

Ala Gly Leu Arg Asp Ala Ile Ala Glu Lys Gly Gly Asp Pro Ala Lys 100 105 110

Val Asn Pro Val Val Ala Lys Pro Ser Phe Ile Val Asp His Ser Leu 115 120 125

Ala Val Glu Cys Gly Gly Tyr Asp Pro Asp Ala Phe Arg Lys Asn Arg 130 135 140

Gln Ile Glu Asp Arg Arg Asn Glu Asp Arg Phe His Phe Ile Asn Trp 145 150 155 160

Thr Lys Thr Ala Phe Glu Asn Val Asp Val Ile Pro Ala Gly Asn Gly 165 170 175

Ile Met His Gln Ile Asn Leu Glu Lys Met Ser Pro Val Val Gln Val 180 185 190

Lys Asn Gly Val Ala Phe Pro Asp Thr Cys Val Gly Thr Asp Ser His 195 200 205

Thr Pro His Val Asp Ala Leu Gly Val Ile Ser Val Gly Val Gly Gly 210 215 220

Leu Glu Ala Glu Thr Val Met Leu Gly Arg Ala Ser Met Met Arg Leu 225 230 235 240

Pro Asp Ile Val Gly Val Glu Leu Asn Gly Lys Arg Gln Ala Gly Ile
245 250 255

Thr Ala Thr Asp Ile Val Leu Ala Leu Thr Glu Phe Leu Arg Lys Glu $260 \hspace{1.5cm} 265 \hspace{1.5cm} 270 \hspace{1.5cm}$

Arg Val Val Gly Ala Phe Val Glu Phe Phe Gly Glu Gly Ala Arg Ser 275 280 285

Leu Ser Ile Gly Asp Arg Ala Thr Ile Ser Asn Met Thr Pro Glu Phe 290 295 300

Gly Ala Thr Ala Ala Met Phe Ala Ile Asp Glu Gln Thr Ile Asp Tyr 305 310 315 320

Leu Lys Leu Thr Gly Arg Asp Asp Ala Gln Val Lys Leu Val Glu Thr \$325\$ \$330 \$335

Tyr Ala Lys Thr Ala Gly Leu Trp Ala Asp Ala Leu Lys Thr Ala Val 340 345 350

Tyr Pro Arg Val Leu Lys Phe Asp Leu Ser Ser Val Thr Arg Asn Met 355 360 365

Ala Gly Pro Ser Asn Pro His Ala Arg Phe Ala Thr Ala Asp Leu Ala 370 380

Ser Lys Gly Leu Ala Lys Pro Tyr Glu Glu Pro Ser Asp Gly Gln Met 385 390 395 400

Pro Asp Gly Ala Val Ile Ile Ala Ala Ile Thr Ser Cys Thr Asn Thr

405 • 410 415

Ser Asn Pro Arg Asn Val Val Ala Ala Ala Leu Leu Ala Arg Asn Ala 420 425 430

Asn Cys Phe Gly Leu Lys Arg Lys Pro Trp Val Lys Thr Ser Phe Ala 435 440 445

Pro Gly Ser Lys Val Ala Glu Ile Tyr Leu Lys Glu Ala Gly Leu Leu 450 460

Pro Glu Met Glu Lys Leu Gly Phe Gly Ile Val Ala Phe Ala Cys Thr 465 470 475 480

Thr Cys Asn Gly Met Ser Gly Ala Leu Asp Pro Lys Ile Gln Lys Glu 485 490 495

Ile Ile Asp Arg Asp Leu Tyr Ala Thr Ala Val Leu Ser Gly Asn Arg 500 505 510

Asn Phe Asp Gly Arg Val His Pro Tyr Ala Lys Gln Ala Phe Leu Ala 515 520 525

Ser Pro Pro Leu Val Val Ala Tyr Ala Leu Ala Gly Ser Ile Arg Phe 530 540

Asp Ile Glu Asn Asp Val Leu Gly Val Ala Asp Gly Lys Glu Ile Arg 545 550 555 560

Leu Lys Asp Ile Trp Pro Ala Asp Glu Glu Ile Asp Ala Val Ala 565 570 575

Glu Tyr Val Lys Pro Gln Gln Phe Arg Asp Val Tyr Val Pro Met Phe 580 585 590

Asp Thr Gly Thr Ala Gln Lys Ala Pro Ser Pro Leu Tyr Asp Trp Arg 595 600 605

Pro Met Ser Thr Tyr Ile Arg Arg Pro Pro Tyr Trp Glu Gly Ala Leu 610 620

Ala Gly Glu Arg Thr Leu Arg Gly Met Arg Pro Leu Ala Ile Leu Pro 625 630 635 640

Asp Asn Ile Thr Thr Asp His Leu Ser Pro Ser Asn Ala Ile Leu Ala 645 650 655

Val Ser Ala Ala Gly Glu Tyr Leu Ala Lys Met Gly Leu Pro Glu Glu 660 665 670

Asp Phe Asn Ser Tyr Ala Thr His Arg Gly Asp His Leu Thr Ala Gln 675 680 685

Arg Ala Thr Phe Ala Asn Pro Lys Leu Phe Asn Glu Met Val Lys Asn 690 695 700

Glu Asp Gly Ser Val Arg Gln Gly Ser Phe Ala Arg Val Glu Pro Glu 705 710 715 720

Gly Glu Thr Met Arg Met Trp Glu Ala Ile Glu Thr Tyr Met Asn Arg
725 730 735

Lys Gln Pro Leu Ile Ile Ile Ala Gly Ala Asp Tyr Gly Gln Gly Ser $740 \hspace{1.5cm} 745 \hspace{1.5cm} 750$

Ser Arg Asp Trp Ala Ala Lys Gly Val Arg Leu Ala Gly Val Glu Ala

The Val Ala Glu Gly Phe Glu Arg Ile His Arg Thr Asn Leu Ile Gly Met Gly Val Leu Pro Leu Gln Phe Lys Pro Asp Thr Asn Arg His Thr 785

Leu Gln Leu Asp Gly Thr Glu Thr Tyr Asp Val Val Gly Glu Arg Thr 805 810 815

Pro Arg Cys Asp Leu Thr Leu Val Ile His Arg Lys Asn Gly Glu Thr 820 825 830

Val Glu Val Pro Val Thr Cys Arg Leu Asp Thr Ala Glu Glu Val Leu $835 \\ 840 \\ 845$

Val Tyr Glu Ala Gly Gly Val Leu Gln Arg Phe Ala Gln Asp Phe Leu 850 860

Glu Gly Asn Ala Ala 865

<210> 43 <211> 1170

<212> DNA

<213> Neisseria meningitidis

<220>

<221> CDS

<222> (1)..(1167)

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gcg gga agc gca cgc gac aaa atc ctc ttg cgc gta ctc ggc agc ccg 144
Ala Gly Ser Ala Arg Asp Lys Ile Leu Leu Arg Val Leu Gly Ser Pro
35 40 45

gac ccc tac ggc aag cag ata gac ggt ttg ggc aac gcc agt tcg tcc 192
Asp Pro Tyr Gly Lys Gln Ile Asp Gly Leu Gly Asn Ala Ser Ser Ser
50 55 60

acc agc aaa gcc gtg att ttg gac aag tcc gaa cgc acc gat cac gat 240 Thr Ser Lys Ala Val Ile Leu Asp Lys Ser Glu Arg Thr Asp His Asp 65 70 75 80

gtc gat tac ctt ttc ggg caa gtt tcc atc gac aaa cct ttt gtc gat 288 Val Asp Tyr Leu Phe Gly Gln Val Ser Ile Asp Lys Pro Phe Val Asp 85 90 95

tgg agt ggc aac tgc ggc aac ctc acc gcc gcc gtg ggc gca ttt gcc 336
Trp Ser Gly Asn Cys Gly Asn Leu Thr Ala Ala Val Gly Ala Phe Ala
100 105 110

atc gag caa ggc ttg gtc gat aaa tcc aaa atc cct tca gac ggc ccg 384
Ile Glu Gln Gly Leu Val Asp Lys Ser Lys Ile Pro Ser Asp Gly Pro
115 120 125

_		_	aaa Lys			-									-	432
	-	_	atg Met				-	_	-	_			_			480
	-		gta Val													528
			gac Asp 180													576
_	-		gat Asp		_				_	_		_	_			624
			att Ile	_		-		_				_	_			672
_			gag Glu	_		-	_				_	_	-	-	_	720
			gag Glu													768
	_	_	gta Val 260		_											816
			gcg Ala													864
			gcc Ala													912
			cac His													960
			gtg Val													1008
			gaa Glu 340													1056
			gcc Ala													1104
gtt Val	atg Met 370	agc Ser	cgc Arg	agc Ser	gca Ala	cgc Arg 375	gtg Val	atg Met	atg Met	gaa Glu	ggt Gly 380	tgg Trp	gtc Val	agg Arg	gtg Val	1152
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<211> 389

<212> PRT

<213> Neisseria meningitidis

<400> 44

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Ala Gly Ser Ala Arg Asp Lys Ile Leu Leu Arg Val Leu Gly Ser Pro 35 40 45

Asp Pro Tyr Gly Lys Gln Ile Asp Gly Leu Gly Asn Ala Ser Ser Ser 50 55 60

Thr Ser Lys Ala Val Ile Leu Asp Lys Ser Glu Arg Thr Asp His Asp 65 70 75 80

Val Asp Tyr Leu Phe Gly Gln Val Ser Ile Asp Lys Pro Phe Val Asp 85 90 95

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Ile Glu Gln Gly Leu Val Asp Lys Ser Lys Ile Pro Ser Asp Gly Pro 115 120 125

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Leu Asp Gly Val Thr Phe Pro Ala Ala Glu Val Gln Ile Glu Phe Leu 165 170 175

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Asn Ala Gly Ile Pro Thr Val Phe Leu Asn Ala Ala Asp Leu Gly Tyr 210 215 220

Thr Gly Lys Glu Leu Gln Asp Asp Ile Asn Asn Asp Ala Ala Ala Leu 225 230 235 240

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Ile Ser Asp Val Ser Glu Ala Ala Ala Arg Ala His Thr Pro Lys Val 260 265 270

Ala Phe Val Ala Pro Ala Ala Asp Tyr Thr Ala Ser Ser Gly Lys Thr 275 280 285

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Pro Pro	Thr	Leu	Leu 200	Ala	Ala	Gly	Asp	Gln 205	Val	Arg	Phe	
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Leu Asp Gly Glu Pro Val Tyr Ser Tyr Trp Arg Tyr Thr Ala Arg Lys
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Gly Gln Thr Leu Lys Met Val Arg Ala Val Gln Gly Met Tyr Gly Tyr $100 \hspace{1.5cm} 105 \hspace{1.5cm} 105 \hspace{1.5cm} 110 \hspace{1.5cm}$

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Gln Lys Gly Asp Tyr Leu Pro Ile Gly Lys Gly Ala Gln Glu Leu Ser 145 150 155 160

Lys Val Gly Ile Ala Pro Ile Pro Phe Thr Asp Thr Ile His Leu Val 165 170 175

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Arg Phe Asp Gly Gln Pro Leu Thr Leu Ser Gln Pro Leu Glu Met Leu 210 215 220

Ser His Ala Val Gln Ala Gly Thr Val Gln Val Pro Pro Gly Gly Lys 225 230 235 240

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	ggc Gly															336
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ggc	ata Ile	cgc Arg	cgc Arg	att Ile 485	ttc Phe	gtc Val	gtt Val	gga Gly	ttg Leu 490	Ser	aca Thr	ggt	tcg Ser	tgg Trp 495		1488
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ccg Pro	ctt Leu 530	ttg Leu	cag Gln	gac Asp	aaa Lys	cgt Arg 535	gtt Val	gaa Glu	att Ile	gta Val	ttg Leu 540	gat Asp	gac Asp	ggt Gly	agg Arg	1632
aaa Lys 545																1680
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atg Met	ttt Phe	aat Asn 595	acc Thr	acg Thr	cac His	agc Ser	ccg Pro 600	cat His	gct Ala	ttt Phe	gct Ala	acc Thr 605	gcc Ala	gta Val	cac His	1824
agt Ser																1872
acc Thr 625	ccg Pro	gta Val	gtt Val	ttc Phe	cct Pro 630	aat Asn	aaa Lys	gaa Glu	ctg Leu	ctc Leu 635	aag Lys	caa Gln	cgt Arg	ctc Leu	tcc Ser 640	1920
cgg Arg	ttg Leu	att Ile	tgg Trp	ccg Pro 645	gaa Glu	agc Ser	ggc Gly	agg Arg	cac His 650	gta Val	ttt Phe	gac Asp	agc Ser	agc Ser 655	acc Thr	1968
gtg Val	gat Asp	gct Ala	gca Ala 660	gca Ala	caa Gln	aag Lys	gtt Val	gtc Val 665	tct Ser	cgt Arg	atg Met	ctg Leu	att Ile 670	cag Gln	atg Met	2016
acg Thr	gaa Glu	cct Pro 675	tcg Ser	gct Ala	ggg	gcg Ala	gaa Glu 680	gtc Val	att Ile	acc Thr	gac Asp	gat Asp 685	aat Asn	atg Met	att Ile	2064
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Leu	Leu	Phe 35		His	Ile	Gly	Ile 40		Leu	Ser	Ser	Ile 45		Val	Ile	
Ile	Ser 50		Phe	Met	Val	Gly 55		Gly	· Val	Gly	Ala 60		Phe	Gly	Gly	

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410

Ser Val Phe Gln Asn Ile Ala Asp Arg Pro Asp Arg Leu Ile Glu Asn 425 Lys His Gly Ile Val Ala Val Tyr His Arg Asp Gly Asp Lys Val Val Tyr Gly Ala Asn Val Tyr Asp Gly Ala Tyr Asn Thr Asp Val Phe Asn Ser Val Asn Gly Ile Glu Arg Ala Tyr Leu Leu Pro Ser Leu Lys Ser 475 Gly Ile Arg Arg Ile Phe Val Val Gly Leu Ser Thr Gly Ser Trp Ala Arg Val Leu Ser Ala Ile Pro Glu Met Gln Ser Met Ile Val Ala Glu 505 Ile Asn Pro Ala Tyr Arg Ser Leu Ile Ala Asp Glu Pro Gln Ile Ala Pro Leu Leu Gln Asp Lys Arg Val Glu Ile Val Leu Asp Asp Gly Arg 535 Lys Trp Leu Arg Arg His Pro Asp Glu Lys Phe Asp Leu Ile Leu Met 555 Asn Thr Trp Tyr Trp Arg Ala Tyr Ser Thr Asn Leu Leu Ser Ala 570 Glu Phe Leu Lys Gln Val Gln Ser His Leu Thr Pro Asp Gly Ile Val 585 Met Phe Asn Thr Thr His Ser Pro His Ala Phe Ala Thr Ala Val His 600 Ser Ile Pro Tyr Ala Tyr Arg Tyr Gly His Met Val Val Gly Ser Ala Thr Pro Val Val Phe Pro Asn Lys Glu Leu Leu Lys Gln Arg Leu Ser 635 Arg Leu Ile Trp Pro Glu Ser Gly Arg His Val Phe Asp Ser Ser Thr Val Asp Ala Ala Gln Lys Val Val Ser Arg Met Leu Ile Gln Met 665

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His Cys Gly Ile Thr Ala Met Trp Cys Leu Ser Ala Pro Tyr Glu Ala 355 360 365

Ser Val Arg Phe Thr Arg Thr Asn Pro Ile Gln Ile Ala Gly Thr Ser , 375 Phe Ser Ala Pro Ile Val Thr Gly Thr Ala Ala Leu Leu Leu Gln Lys 390 395 Tyr Pro Trp Met Ser Asn Asp Asn Leu Arg Thr Thr Leu Leu Thr Thr 410 Ala Gln Asp Ile Gly Ala Val Gly Val Asp Ser Lys Phe Gly Trp Gly 425 Leu Leu Asp Ala Gly Lys Ala Met Asn Gly Pro Ala Ser Phe Pro Phe 440 Gly Asp Phe Thr Ala Asp Thr Lys Gly Thr Ser Asp Ile Ala Tyr Ser 455 Phe Arg Asn Asp Ile Ser Gly Thr Gly Gly Leu Ile Lys Lys Gly Gly 470 475 Ser Gln Leu Gln Leu His Gly Asn Asn Thr Tyr Thr Gly Lys Thr Ile 490 Ile Glu Gly Gly Ser Leu Val Leu Tyr Gly Asn Asn Lys Ser Asp Met 505 Arg Val Glu Thr Lys Gly Ala Leu Ile Tyr Asn Gly Ala Ala Ser Gly Gly Ser Leu Asn Ser Asp Gly Ile Val Tyr Leu Ala Asp Thr Asp Arg 535 Ser Gly Ala Asn Glu Thr Val His Ile Lys Gly Asp Leu Gln Leu Gly 550 Gly Glu Gly Thr Leu Tyr Thr Arg Leu Gly Lys Leu Leu Lys Val Asp 570 Gly Thr Ala Met Thr Gly Gly Lys Leu Tyr Met Ser Ala Arg Gly Lys 585 580 Gly Ala Gly Tyr Leu Asn Arg Thr Gly Gln Arg Val Pro Phe Leu Ser 600 Ala Ala Lys Ile Gly Arg Asp Tyr Ser Phe Phe Thr Asn Ile Glu Thr 615 Asp Gly Gly Leu Leu Ala Ser Leu Asp Ser Val Glu Lys Thr Ala Gly 635 630 Ser Glu Gly Asp Thr Leu Ser Tyr Tyr Val Arg Arg Gly Asn Ala Ala Arg Thr Ala Ser Ala Ala Ala His Ser Ala Pro Ala Gly Leu Lys His Ala Val Glu Gln Gly Gly Ser Asn Leu Glu Asn Leu Met Val Glu Leu Asp Ala Ser Glu Ser Ser Ala Thr Pro Glu Thr Val Glu Thr Ala Ala Ala Asp Arg Thr Asp Met Pro Gly Ile Arg Pro Tyr Gly Ala Thr Phe

- Arg Ala Ala Ala Val Gln His Ala Asn Ala Ala Asp Gly Val Arg Ile Phe Asn Ser Leu Ala Ala Thr Val Tyr Ala Asp Ser Thr Ala Ala 745 His Ala Asp Met Gln Gly Arg Arg Leu Lys Ala Val Ser Asp Gly Leu Asp His Asn Ala Thr Gly Leu Arg Val Ile Ala Gln Thr Gln Gln Asp 775 Gly Gly Thr Trp Glu Gln Gly Gly Val Glu Gly Lys Met Arg Gly Ser Thr Gln Thr Val Gly Ile Ala Ala Lys Thr Gly Glu Asn Thr Thr Ala Ala Ala Thr Leu Gly Met Gly His Ser Thr Trp Ser Glu Asn Ser Ala Asn Ala Lys Thr Asp Ser Ile Ser Leu Phe Ala Gly Ile Arg His Asp Ala Gly Asp Ile Gly Tyr Leu Lys Gly Leu Phe Ser Tyr Gly Arg Tyr Lys Asn Ser Ile Ser Arg Ser Thr Gly Ala Asp Glu His Ala Glu Gly Ser Val Asn Gly Thr Leu Met Gln Leu Gly Ala Leu Gly Gly Val Asn Val Pro Phe Ala Ala Thr Gly Asp Leu Thr Val Glu Gly Gly Leu Arg Tyr Asp Leu Leu Lys Gln Asp Ala Phe Ala Glu Lys Gly Ser Ala Leu Gly Trp Ser Gly Asn Ser Leu Thr Glu Gly Thr Leu Val Gly Leu Ala Gly Leu Lys Leu Ser Gln Pro Leu Ser Asp Lys Ala Val Leu Phe Ala 955 Thr Ala Gly Val Glu Arg Asp Leu Asn Gly Arg Asp Tyr Thr Val Thr Gly Gly Phe Thr Gly Ala Thr Ala Ala Thr Gly Lys Thr Gly Ala Arg Asn Met Pro His Thr Arg Leu Val Ala Gly Leu Gly Ala Asp Val Glu

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Lys Gln Tyr Gly Asn His Ser Gly Arg Val Gly Val Gly Tyr Arg Phe 1035 1025

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cat His	ttg Leu	ggt Gly	gta Val 20	aag Lys	atg Met	tat Tyr	tcg Ser	cac His 25	act Thr	gtt Val	cct Pro	gcg Ala	att Ile 30	gcc Ala	gag Glu	96
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Ala 225	Thr	Asn	Ile	Ser	Ser 230	Leu •	Ser	Ser	Lys	Phe 235	Glu	Gln	Tyr	Glu	Tyr 240
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	ccc Pro												taa		
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Met 1	Ser	GIU	GIU	Lys 5	Leu	ьys	мет	ser	10	GIU	PIO	1111	val	15	Giu
His	Leu	Gly	Val 20	Lys	Met	Tyr	Ser	His 25	Thr	Val	Pro	Ala	Ile 30	Ala	Glu
Leu	Ile	Ala 35_		Ala	Tyr	Asp	Ala 40	Cys	Ala	Thr	Glu	Val 45	Glu	Val	Arg
Leu	Phe 50	Asp	Lys	Pro	Glu	His 55	Lys	Ile	Val	Ile	Lys 60	Asp	Asn	Gly	Ile
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Asn	Arg	Arg	Glu	Glu 85	Lys	Gln	Ala	Ser	Pro 90	Cys	Gly	Arg	Ile	Pro 95	Thr
Gly	Lys	Lys	Gly 100	Leu	Gly	Lys	Leu	Ala 105	Leu	Phe	Arg	Leu	Gly 110	Asn	Lys
Ile	Glu	Ile 115	Ser	Thr	Ile	Gln	Gly 120	Asn	Glu	Arg	Val	Thr 125	Phe	Thr	Leu
Asp	Tyr 130	Ala	Glu	Ile	Lys	Lys 135	Ser	Glu	Arg	Ile	Tyr 140	Gln	Pro	Glu	Phe
Gln 145	Lys	Glu	Ser	Val	Lys 150	Pro	Asn	Thr	Glu	Asn 155	Gly	Thr	Thr	Ile	Thr 160
Leu	Thr	Glu	Leu	Thr 165	Lys	Lys	Gln	Gly	Tyr 170		Leu	Asp	Asn	Tyr 175	
Gly	His	Leu	Ser 180	Arg	Leu	Phe	Asp	Phe 185		Ala	Gln	Asp	Phe 190	Lys	Ile
Lys	Val	Ser 195		Asn	Gly	Ser	Glu 200		Arg	Ile	Ile	Asp 205		Asn	Leu
Lys	Tyr 210		Leu	Val	Thr	Pro 215		Phe	Glu	Trp	Glu 220		Gln	Asp	Leu
Ala 225		Asn	Ile	Ser	Ser 230		Ser	Ser	Lys	Phe 235		Gln	Tyr	Glu	Tyr 240

Ser Gly Leu	Ile Gln 245	Gly Lys	Phe Ile	Thr Th 250	r Glu L	ys Pro	Leu : 255	Lys	
Asn Asn Met	Lys Gly 260	Ile Thr	Leu Phe 265	Ala As	n Gly A	rg Met 270	Val 1	Asn	
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acc gaa gtc Thr Glu Val	ggc agc Gly Ser 100	gcg ggc Ala Gly	gcg tcg Ala Ser 105	Met Le	g gat a u Asp L	ag ttg ys Leu 110	tgg Trp	ctg Leu	336
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aag ttc cgc Lys Phe Arg 130	cgt aag Arg Lys	acg cat Thr His 135	ttt tct Phe Ser	gcc ga Ala As	at ata c sp Ile I 140	tg ttt eu Phe	gcc Ala	ttc Phe	432
cta atg ctg Leu Met Leu	Met Ile	ttc gtg Phe Val	cgt tcg Arg Ser	ttc ga	sp Thr I	aa caa .ys Gln	gag Glu	cac His 160	480

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				cct Pro												624
				caa Gln												672
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gtc Val	ata Ile	ccg Pro 275	cac His	gcc Ala	aac Asn	ggc Gly	ttg Leu 280	gaa Glu	caa Gln	atc Ile	agc Ser	ggc Gly 285	ggc Gly	gat Asp	acc Thr	864
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cac	gcc Ala 370	cca Pro	tac Tyr	ggc	gca Ala	ttg Leu 375	ttg Leu	cag Gln	cct Pro	caa Gln	gat Asp 380	aaa Lys	gta Val	ttc Phe	ggc Gly	1152
gaa Glu 385	gcc Ala	gat Asp	att Ile	gtg Val	gat Asp 390	Lys	tac Tyr	gac Asp	aac Asn	acc Thr 395	Ile	cac His	aaa Lys	acc Thr	gac Asp 400	1200
caa Gln	atg Met	att Ile	caa Gln	acc Thr 405	Val	ttc Phe	gag Glu	cag Gln	ctg Leu 410	Gln	aag Lys	cag Gln	cct Pro	gac Asp 415	ggc	1248
aac Asn	tgg Trp	ctg Leu	ttt Phe 420	Ala	tat Tyr	acc Thr	tcc Ser	gat Asp 425	His	ggc Gly	cag Gln	tat Tyr	gtg Val 430	. Arg	caa Gln	1296
gat Asp	atc Ile	tac Tyr	aat Asn	caa Gln	ggc	acg Thr	gtg Val	caq Glr	ccc Pro	gac Asp	ago Ser	tat Tyr	att Ile	gtg Val	cct Pro	1344

	ttg Leu							cag Gln	1392
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Ala Ala Lys Met Ala Glu Thr Phe Ala Leu Thr Phe Met Ile Ala Ala 40

Leu Tyr Leu Phe Ala Arg Tyr Lys Ala Ser Arg Leu Leu Ile Ala Val

Phe Phe Ala Phe Ser Met Ile Ala Asn Asn Val His Tyr Ala Val Tyr

Gln Ser Trp Met Thr Gly Ile Asn Tyr Trp Leu Met Leu Lys Glu Val

Thr Glu Val Gly Ser Ala Gly Ala Ser Met Leu Asp Lys Leu Trp Leu

Pro Ala Leu Trp Gly Val Ala Glu Val Met Leu Phe Cys Ser Leu Ala

Lys Phe Arg Arg Lys Thr His Phe Ser Ala Asp Ile Leu Phe Ala Phe 135

Leu Met Leu Met Ile Phe Val Arg Ser Phe Asp Thr Lys Gln Glu His 150 155

Gly Ile Ser Pro Lys Pro Thr Tyr Ser Arg Ile Lys Ala Asn Tyr Phe 170

Ser Phe Gly Tyr Phe Val Gly Arg Val Leu Pro Tyr Gln Leu Phe Asp 190 185

Leu Ser Lys Ile Pro Val Phe Lys Gln Pro Ala Pro Ser Lys Ile Gly

Gln Gly Ser Ile Gln Asn Ile Val Leu Ile Met Gly Glu Ser Glu Ser 210 215 220

Ala Ala His Leu Lys Leu Phe Gly Tyr Gly Arg Glu Thr Ser Pro Phe 225 230 235 240

Leu Thr Arg Leu Ser Gln Ala Asp Phe Lys Pro Ile Val Lys Gln Ser 245 250 255

Tyr Ser Ala Gly Phe Met Thr Ala Val Ser Leu Pro Ser Phe Phe Asn 260 265 270

Val Ile Pro His Ala Asn Gly Leu Glu Gln Ile Ser Gly Gly Asp Thr 275 280 285

Asn Met Phe Arg Leu Ala Lys Glu Gln Gly Tyr Glu Thr Tyr Phe Tyr 290 295 300

Ser Ala Gln Ala Glu Asn Gln Met Ala Ile Leu Asn Leu Ile Gly Lys 305 310 315

Lys Trp Ile Asp His Leu Ile Gln Pro Thr Gln Leu Gly Tyr Gly Asn 325 330 335

Gly Asp Asn Met Pro Asp Glu Lys Leu Leu Pro Leu Phe Asp Lys Ile 340 345 350

Asn Leu Gln Gln Gly Arg His Phe Ile Val Leu His Gln Arg Gly Ser 355 360 365

His Ala Pro Tyr Gly'Ala Leu Leu Gln Pro Gln Asp Lys Val Phe Gly 370 375 380

Glu Ala Asp Ile Val Asp Lys Tyr Asp Asn Thr Ile His Lys Thr Asp 385 390 395 400

Gln Met Ile Gln Thr Val Phe Glu Gln Leu Gln Lys Gln Pro Asp Gly
405 410 415

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Asp Ile Tyr Asn Gln Gly Thr Val Gln Pro Asp Ser Tyr Ile Val Pro 435 445

Leu Val Leu Tyr Ser Pro Asp Lys Ala Val Gln Gln Ala Ala Asn Gln 450 455 460

Ala Phe Ala Pro Cys Glu Ile Ala Phe His Gln Gln Leu Ser Thr Phe 465 470 475 480

Leu Ile His Thr Leu Gly Tyr Asp Met Pro Val Ser Gly Cys Arg Glu 485 490 495

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ccg Pro	ggt Gly	tat Tyr	gta Val 260	ttt Phe	atg Met	ctg Leu	gct Ala	gca Ala 265	acg Thr	gcg Ala	gcg Ala	ttg Leu	ctt Leu 270	ttg Leu	aat Asn	816
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gcg Ala	tgg Trp	ggt Gly	ttg Leu 420	Ser	ctg Leu	gcg Ala	g ata Ile	ttg Leu 425	. Val	: agt : Ser	tcg Ser	ata Ile	gcg Ala 430	, Ala	gga Gly	1296
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- Leu Ile Gly Ala Leu Leu Ala Gly Phe Asp Val Ser Gln Leu Lys Glu 35 ' 40 45
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- Ala Val Ser Val Gly Thr Val Leu Val Ser Val Val Ala Gln Leu Asp 100 105 110
- Gly Ala Gly Ala Thr Thr Phe Leu Ser Val Val Pro Ala Leu Leu Pro $115 \\ 120 \\ 125$
- Leu Tyr Lys Arg Leu His Met Asn Pro Tyr Leu Leu Phe Leu Leu Leu 130 135 140
- Thr Ser Ser Ala Gly Leu Ile Asn Leu Leu Pro Arg Gly Gly Pro Ile 145 150 155 160
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- Ser Leu Phe Leu Gly Val Arg Glu Lys Arg Arg Ile Val Arg Glu Leu 195 200 205
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 Ser Leu Val Tyr Asn His Ile Asn Asn Glu Pro Phe Ser Asp His Ile
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 Ala Arg Gln Val Ala Arg Phe Ala Gly Ala His Thr Ile Val Ser Gly
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         115
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 Tyr Leu Ala Phe Gly Ser Asp Glu Ser Tyr Lys Asn His Trp Asp Thr
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150

480

Thr	Ala	Pro	Asp	Phe 165	Pro	Met	Pro	Leu	Tyr 170	Met	Gln	Gln	Thr	Lys 175	Asp	
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				ctc Leu												624
				gaa Glu												672
				tac Tyr												720
				cac His 245												768
				gcc Ala												816
	Tyr			ttc Phe												864
				ctc Leu												912
				agg Arg												960
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				gtg Val												1056
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met	ъ±У	тте	nlS	Leu	ASP	FIIE	GTÀ	тте	Set	LIO	ъдз	TIIT	FILE	719	GIII	

Met Gly Ile His Leu Asp Phe Gly Ile Ser Pro Lys Thr Phe Arg Gln 1 5 10 15

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		aag Lys														336
		cag Gln 115														384
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cgc Arg 145	agc Ser	ctt Leu	aaa Lys	gca Ala	act Thr 150	gtc Val	gaa Glu	cgt Arg	ttg Leu	gaa Glu 155	aac Asn	cag Gln	gaa Glu	ctc Leu	cat His 160	480
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		ttg Leu														576
		gaa Glu														624

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Ser Val Gln Gln Gln Leu Lys Thr Glu Ala Val Leu Lys Lys Thr Leu
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120
125

Ala Glu Glu Leu Gly Arg Leu Lys Leu Ile His Gly Asn Glu Thr 130 135 140

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Ile Ser Gl
n Gl
n Ile Asp Gly Gl
n Lys Arg Arg Ile Arg Leu Ala Glu
 165 170 175

Glu Met Leu Gln Lys Tyr Arg Phe Leu Ser Ala Asn Asp Ala Val Pro 180 185 190

Lys Gln Glu Met Met Asn Val Lys Ala Glu Leu Leu Glu Gln Lys Ala 195 200 205

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Gln Leu Glu Arg Thr Met Ala Asp Ile Ser Gln Glu Val Leu Asp Phe 50 55 60

Glu Met Arg Ser Glu Gln Ile Ile Arg Ala Gly Arg Ser Gly Tyr Ile
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Ala Ile Pro Asn Val Glu Val Gly Arg Gln Val Asp Pro Ser Lys Leu 85 90 95

Leu Leu Ser Ile Val Pro Glu Arg Thr Glu Leu Tyr Ala His Leu Tyr 100 105 110

Ile Pro Ser Ser Ala Ala Gly Phe Ile Lys Pro Lys Asp Lys Val Val 115 120 125

Leu Arg Tyr Gln Ala Tyr Pro Tyr Gln Lys Phe Gly Leu Ala Ser Gly 130 135 140

Ser Val Val Ser Val Ala Lys Thr Ala Leu Gly Arg Gln Glu Leu Ser 145 150 155 160

Gly Leu Gly Met Val Ser Ser Asp Leu Ala Lys Ser Asn Glu Pro Val 165 170 175

Tyr Leu Val Lys Ile Lys Pro Asp Lys Pro Thr Ile Thr Ala Tyr Gly 180 185 190

Glu Glu Lys Pro Leu Gln Ile Gly Met Thr Leu Glu Ala Asp Ile Leu 195 200 205

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aat Asn	aat Asn	ttc Phe	ggg Gly 20	ttt Phe	ttg Leu	cgc Arg	ctg Leu	ccg Pro 25	ctt Leu	aat Asn	ttt Phe	atg Met	ccg Pro 30	tat Tyr	gaa Glu	96
	cat His															144
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924

260

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Gln Arg Asp Ala Val Arg A	Ala Arg Gln Glr 90		Ala Phe 95
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Thr Leu Phe Asp Ala Ala 1	Lys Phe Ala Glr 135	n Tyr Arg Gln Ser 140	Arg Phe
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Leu Leu Lys Val Ala Glu 165	Ser Tyr Phe Asi		Arg Asp 175
Thr Val Ala Ala His Ala 180	Ala Glu Lys Gl ^e 185	u Ala Tyr Ala Glr 190	n Gln Val
Arg Gln Ala Gln Ala Leu 195	Phe Asn Lys Gl 200	y Ala Ala Thr Ala 205	a Leu Asp
Ile His Glu Ala Lys Ala 210	Gly Tyr Asp As 215	n Ala Leu Ala Glr 220	n Glu Ile
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Thr Asp Leu Asp Ser Lys Gln Ile Glu Ala Ile Asp Thr Ala Asn Leu 250 Leu Ala Arg Tyr Leu Pro Lys Leu Glu Arg Tyr Ser Leu Asp Glu Trp 265 Gln Arg Ile Ala Leu Ser Asn Asn His Glu Tyr Arg Met Gln Gln Leu Ala Leu Gln Ser Ser Gly Gln Ala Leu Arg Ala Ala Gln Asn Ser Arg Tyr Pro Thr Val Ser Ala His Val Gly Tyr Gln Asn Asn Leu Tyr Thr 315 Ser Ser Ala Gln Asn Asn Asp Tyr His Tyr Arg Gly Lys Gly Met Ser Val Gly Val Gln Leu Asn Leu Pro Leu Tyr Thr Gly Gly Glu Leu Ser 345 Gly Lys Ile His Glu Ala Glu Ala Gln Tyr Gly Ala Ala Glu Ala Gln Leu Thr Ala Thr Glu Arg His Ile Lys Leu Ala Val Arg Gln Ala Tyr 375 Thr Glu Ser Gly Ala Ala Arg Tyr Gln Ile Met Ala Gln Glu Arg Val 395 Leu Glu Ser Ser Arg Leu Lys Leu Lys Ser Thr Glu Thr Gly Gln Gln Tyr Gly Ile Arg Asn Arg Leu Glu Val Ile Arg Ala Arg Gln Glu Val Ala Gln Ala Glu Gln Lys Leu Ala Gln Ala Arg Tyr Lys Phe Met Leu Ala Tyr Leu Arg Leu Val Lys Glu Ser Gly Leu Gly Leu Glu Thr Val 460 Phe Ala Glu 465 <210> 70 <211> 696 <212> DNA <213> Neisseria gonorrhoeae <220> <221> CDS <222> (1)..(693) <400> 70 atg aaa caa tcc gcc cga ata aaa aat atg gat cag aca tta aaa aat 48 Met Lys Gln Ser Ala Arg Ile Lys Asn Met Asp Gln Thr Leu Lys Asn

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ego Arg	tgc g Cys	gac Asp	cto Lev 820	ı Thr	ctt Leu	gto Val	att . Ile	cac His 825	Arg	aaa g Lys	a aac s Asr	ggc Gly	gag Glu 830	ı Thi	gtc Val	2496
gaa Glu	a gto ı Val	e ccc Pro 835) Ile	aco Thr	tgc Cys	c cgc s Arg	c cto Leu 840	ı Asp	aco Thi	c gca r Ala	a gaa a Glu	gaa Glu 845	ı Val	tto Lev	g gta ı Val	2544
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Asn Arg Ala Asp Lys Val Asp Leu Pro Thr Leu Gln Ser Trp Leu Gly 50 55 60

Gln Leu Ile Glu Gly Lys Gln Glu Ile Asp Phe Pro Trp Tyr Pro Ala 65 70 75 80

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Ala Gly Leu Arg Asp Ala Ile Ala Glu Lys Gly Gly Asp Pro Ala Lys
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Ile Glu Asp Arg Arg Asn Glu Asp Arg Phe His Phe Ile Asn Trp Thr

Lys Thr Ala Phe Glu Asn Val Asp Val Ile Pro Ala Gly Asn Gly Ile 165 170 175

Met His Gln Ile Asn Leu Glu Lys Met Ser Pro Val Val Gln Val Lys 180 185 190

Asn Gly Val Ala Phe Pro Asp Thr Cys Val Gly Thr Asp Ser His Thr 195 200 205

Pro His Val Asp Ala Leu Gly Val Ile Ser Val Gly Val Gly Gly Leu 210 215 220

Glu Ala Glu Thr Val Met Leu Gly Arg Ala Ser Met Met Arg Leu Pro 225 230 235 240

Asp Ile Val Gly Val Glu Leu Asn Gly Lys Arg Lys Ala Gly Ile Thr

Ala Thr Asp Ile Val Leu Ala Leu Thr Glu Phe Leu Arg Lys Glu Arg 260 265 270

Val Val Gly Ala Phe Val Glu Phe Phe Gly Glu Gly Ala Arg Ser Leu 275 280 285

Ser Ile Gly Asp Arg Ala Thr Ile Ser Asn Met Thr Pro Glu Phe Gly 2.95 Ala Thr Ala Ala Met Phe Ala Ile Asp Glu Gln Thr Ile Asp Tyr Leu 315 Lys Leu Thr Gly Arg Asp Asp Ala Gln Val Lys Leu Val Glu Thr Tyr 330 Ala Lys Thr Ala Gly Leu Trp Ala Asp Ala Leu Lys Thr Ala Val Tyr 345 Pro Arg Val Leu Lys Phe Asp Leu Ser Ser Val Thr Arg Asn Met Ala 360 Gly Pro Ser Asn Pro His Ala Arg Phe Ala Thr Ala Asp Leu Ala Gly Lys Gly Leu Ala Lys Pro Tyr Glu Glu Pro Ser Asp Gly Gln Met Pro 395 Asp Gly Ala Val Ile Ile Ala Ala Ile Thr Ser Cys Thr Asn Thr Ser Asn Pro Arg Asn Val Val Ala Ala Ala Leu Leu Ala Arg Asn Ala Asn Arg Leu Gly Leu Gln Arg Lys Pro Trp Val Lys Ser Ser Phe Ala Pro Gly Ser Lys Val Ala Glu Ile Tyr Leu Lys Glu Ala Asp Leu Leu Pro Glu Met Glu Lys Leu Gly Phe Gly Ile Val Ala Phe Ala Cys Thr Thr 475 Cys Asn Gly Met Ser Gly Ala Leu Asp Pro Lys Ile Gln Lys Glu Ile 490 Ile Asp Arg Asp Leu Tyr Ala Thr Ala Val Leu Ser Gly Asn Arg Asn 505 Phe Asp Gly Arg Ile His Pro Tyr Ala Lys Gln Ala Phe Leu Ala Ser 520 Pro Pro Leu Val Val Ala Tyr Ala Leu Ala Gly Ser Ile Arg Phe Asp 535 Ile Glu Asn Asp Val Leu Gly Val Ala Asp Gly Lys Glu Ile Arg Leu 555 550 Lys Asp Ile Trp Pro Thr Asp Glu Glu Ile Asp Ala Ile Val Ala Glu 565 Tyr Val Lys Pro Gln Gln Phe Arg Asp Val Tyr Ile Pro Met Phe Asp Thr Gly Thr Ala Gln Lys Ala Pro Ser Pro Leu Tyr Asp Trp Arg Pro 600 Met Ser Thr Tyr Ile Arg Arg Pro Pro Tyr Trp Glu Gly Ala Leu Ala 615

Gly Glu Arg Thr Leu Ser Gly Met Arg Pro Leu Ala Ile Leu Pro Asp

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Phe Asn Ser Tyr Ala Thr His Arg Gly Asp His Leu Thr Ala Gln Arg
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Ala Thr Phe Ala Asn Pro Lys Leu Phe Asn Glu Met Val Arg Asn Glu
                         695
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Gln Thr Met Arg Met Trp Glu Ala Ile Glu Thr Tyr Met Asn Arg Lys
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Val Ala Glu Gly Phe Glu Arg Ile His Arg Thr Asn Leu Ile Gly Met
Gly Val Leu Pro Leu Gln Phe Lys Pro Gly Thr Asn Arg His Thr Leu
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20

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gat Asp	ccc Pro 50	tac Tyr	ggc Gly	aag Lys	cag Gln	ata Ile 55	gac Asp	ggt Gly	ttg Leu	ggc Gly	aac Asn 60	gcc Ala	agc Ser	tcg Ser	tcc Ser	192
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gat Asp	cca Pro	gcc Ala	gac Asp 180	ggc Gly	gaa Glu	ggc	agt Ser	atg Met 185	ttc Phe	cca Pro	acc Thr	ggc Gly	aat Asn 190	ttg Leu	gtc Val	576
gat Asp	gaa Glu	att Ile 195	gat Asp	gtg Val	ccg Pro	aat Asn	ata Ile 200	ggc Gly	cgt Arg	ttg Leu	aaa Lys	gcc Ala 205	Thr	ctc Leu	atc Ile	624
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acg Thr 225	Gly	aaa Lys	gag Glu	ttg Leu	caa Gln 230	gac Asp	gac Asp	atc Ile	aac	aac Asn 235	Asp	gcc Ala	gca Ala	gct Ala	ttg Leu 240	720
gaa Glu	aaa Lys	ttc Phe	gag Glu	aaa Lys 245	Ile	egc Arg	gct Ala	tac Tyr	ggt Gl _y 250	/ Ala	ctg Leu	ı aaa ı Lys	atg Met	ggt Gly 255	ctg Leu	768
ato Ile	ago Ser	gac Asp	gta Val 260	Ser	gaa Glu	gct Ala	gco Ala	gco Ala 265	Arg	g gcg g Ala	g cac a His	aco Thr	g ccg Pro 270	ь гуз	gtc Val	816
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gto Val	g aat L Asr	gco n Ala	e geo a Ala	c gad a Asp	ato Ile	gat Asp	tto Lei	g cto 1 Leo	g gta ı Val	a cgo	e geo g Ala	c cto	g ago ı Sei	ato Met	g ggc Gly	912

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Thr Ser Lys Ala Val Ile Leu Asp Lys Ser Glu Arg Ala Asp His Asp 70

Val Asp Tyr Leu Phe Gly Gln Val Ser Ile Asp Lys Pro Phe Val Asp 85

Trp Ser Gly Asn Cys Gly Asn Leu Thr Ala Ala Val Gly Ala Phe Ala 105 100

Ile Glu Gln Gly Leu Val Asp Lys Gly Lys Ile Pro Ser Asp Gly Ile 120 115

Cys Thr Val Lys Ile Trp Gln Lys Asn Ile Gly Lys Thr Ile Ile Ala 135 130

His Val Pro Met Gln Asn Gly Ala Val Leu Glu Thr Gly Asp Phe Glu 145

Leu Asp Gly Val Thr Phe Pro Ala Ala Glu Val Gln Ile Glu Phe Leu 165 170

Asp Pro Ala Asp Gly Glu Gly Ser Met Phe Pro Thr Gly Asn Leu Val 185 Asp Glu Ile Asp Val Pro Asn Ile Gly Arg Leu Lys Ala Thr Leu Ile 200 Asn Ala Gly Ile Pro Thr Val Phe Leu Asn Ala Ala Asp Leu Gly Tyr 215 Thr Gly Lys Glu Leu Gln Asp Asp Ile Asn Asn Asp Ala Ala Leu 235 Glu Lys Phe Glu Lys Ile Arg Ala Tyr Gly Ala Leu Lys Met Gly Leu 250 Ile Ser Asp Val Ser Glu Ala Ala Ala Arg Ala His Thr Pro Lys Val 265 Ala Phe Val Ala Pro Ala Ala Asp Tyr Thr Ala Ser Ser Gly Lys Thr 280 Val Asn Ala Ala Asp Ile Asp Leu Leu Val Arg Ala Leu Ser Met Gly Lys Leu His His Ala Met Met Gly Thr Ala Ser Val Ala Ile Ala Thr 315 305 Ala Ala Ala Val Pro Gly Thr Leu Val Asn Leu Ala Ala Gly Gly Gly 330 Thr Arg Lys Glu Val Arg Phe Gly His Pro Ser Gly Thr Leu Arg Val 345 Gly Ala Ala Ala Glu Cys Gln Asp Gly Gln Trp Thr Ala Thr Lys Ala 360 Val Met Ser Arg Ser Ala Arg Val Met Met Glu Gly Trp Val Arg Val 375 Pro Glu Asp Cys Phe 385 <210> 76 <211> 2094 <212> DNA <213> Neisseria gonorrhoeae <220> <221> CDS <222> (1)..(2091) <400> 76 48 atg aat tog acc gca agt aaa acc ctg aaa gga ttg tog ctg gtg ttt Met Asn Ser Thr Ala Ser Lys Thr Leu Lys Gly Leu Ser Leu Val Phe tto goo tot ggo tto tgo goo etg att tac cag gto ago tgg cag agg 96 Phe Ala Ser Gly Phe Cys Ala Leu Ile Tyr Gln Val Ser Trp Gln Arg 20 ctt cta ttc agc cac ata ggt atc gat ttg agt tcg att act gtc att 144 Leu Leu Phe Ser His Ile Gly Ile Asp Leu Ser Ser Ile Thr Val Ile 40

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ato Ile	c gcc e Ala	gto Val	ggc Gl ₃ 260	, Ala	tat Tyr	ttt Phe	ggc Gly	aaa Lys 265	Arc	g att g Ile	tgc Cys	e ego s Aro	ago g Ser 270	Arc	ttt Phe	816
gti Va	: gat l Asp	att 5 Ile 275	e Pro	ttt Phe	ato E Ile	e Gly	g caç 7 Glr 280	ı Cys	tto Phe	c tto e Leu	g tgg ı Trp	g gcg Ala 285	a GTZ	att / Ile	gcc Ala	864
ga: Asj	t tti p Phe 29	e Lev	g att	t ttg e Lei	g ggt ı Gly	get Ala 295	a Ala	g tgg a Trp	g tto Le	g tto u Lei	g acq 1 Thi 300	r GI	t ttt y Phe	tcc Ser	c ggt r Gly	912
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ccg ctt ttg cag gac aaa cgt gtt gaa att gta ttg gat gac ggt agg 1632 Pro Leu Leu Gln Asp Lys Arg Val Glu Ile Val Leu Asp Asp Gly Arg 535 530 aaa tgg ctg cgt cgc cat cct gat gaa aaa ttc gac ctg att ttg atg 1680 Lys Trp Leu Arg Arg His Pro Asp Glu Lys Phe Asp Leu Ile Leu Met 555 550 545

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Asn Ser Thr Trp Tyr Trp Arg Ala Tyr Ser Thr Asn Leu Leu Ser Ala

565

570

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Pro Leu Leu Gln Asp Lys Arg Val Glu Ile Val Leu Asp Asp Gly Arg
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Lys Trp Leu Arg Arg His Pro Asp Glu Lys Phe Asp Leu Ile Leu Met
Asn Ser Thr Trp Tyr Trp Arg Ala Tyr Ser Thr Asn Leu Leu Ser Ala
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(54) Titre: ACIDES NUCLEIQUES ET POLYPEPTIDES SPECIFIQUES DES SOUCHES PATHOGENES DU GENRE NEISSERIA

(57) Abstract

The invention concerns nucleic acids coding for polypeptides specific of the *Neisseria* genus pathogenic strains, the corresponding polypeptides, and their diagnostic and therapeutic applications.

(57) Abrégé

Cette invention concerne des acides nucléiques codant pour les polypeptides spécifiques des souches pathogènes du genre Neisseria, les polypeptides correspondants, et leurs applications diagnostiques et thérapeutiques.

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Nucleic acids and polypeptides specific for pathogenic strains of the Neisseria genus.

The present invention relates to nucleic acids encoding polypeptides specific for pathogenic strains of the Neisseria genus, in particular which are useful for preventing or treating a Neisseria meningitidis infection.

In general, meningitis is either of viral origin or of bacterial origin. The bacteria mainly responsible are: type b Haemophilus influenzae, Neisseria meningitidis and Streptococcus pneumoniae. The Neisseria meningitidis species is subdivided into serogroups according to the nature of the capsular polysaccharides. Although about a dozen serogroups exist, 90% of meningitis cases can be attributed to three serogroups: A, B and C.

Effective vaccines based on capsular polysaccharides exist for preventing meningitis caused by Neisseria meningitidis serogroups A and C. These polysaccharides, unmodified, are only slightly immunogenic, or not at all, in children under the age of two, and do not induce any immune memory. However, these drawbacks can be overcome by conjugating these polysaccharides to a carrier protein.

On the other hand, the polysaccharide of Neisseria meningitidis serogroup B is non-immunogenic, or relatively non-immunogenic in humans, whether or not it is in a conjugated form. Thus, it appears to be highly desirable to seek a vaccine against meningitis caused by Neisseria meningitidis, in particular Neisseria meningitidis serogroup B, other than a vaccine based on polysaccharide.

To this end, various proteins of the external membrane of N. meningitidis have already been proposed, such as the membrane-bound receptor for human transferrin (WO 90/12591 and WO 93/06861).

Neisseria meningitidis is genetically very close to Neisseria gonorrhoeae and Neisseria lactamica.

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N. gonorrhoeae is especially responsible for infections located in the urogenital tract. It colonizes the genital mucous membrane, crosses the epithelium and then invades the sub-epithelium, where it multiplies and is responsible for a severe inflammatory reaction. On the other hand, N. lactamica is considered to be a nonpathogenic species.

Sequences present in N. gonorrhoeae and N. meningitidis, but absent from N. lactamica, have been disclosed in patent application WO 98/02547, but this prior patent application does not locate or identify the coding sequences.

The authors of the present invention have now managed to identify some of these genes by searching, in the meningococcal genome, for the open reading frames specific for pathogenic strains of the *Neisseria* genus, using the following strategy:

the sequences disclosed in patent of application WO 98/02547 (referred to, in said prior application, as SEQ ID Nos 66, 67, 69, 70, 72 to 96, 98 and 99) were positioned on the sequence of the genome of the N. meningitidis serogroup B strain (ATCC 13090), available from the Pathoseq® bank of Incyte Pharmaceuticals, and also on the sequence of the genome of the Neisseria meningitidis strain Z2491 Centre). This made it possible to identify, in the N. meningitidis genome which has 2.3 mega bases, 19 contigs representing 220 000 base pairs.

The authors of the present invention then analysed, for each of the 19 contigs, the presence of open reading frames (ORFs) containing at least 100 amino acids (and, by definition, bordered by an initiation codon and a stop codon), using the Gene Jockey II sequence processor® program (Biosoft). This analysis made it possible to select approximately 400 candidate ORFs.

The sequences of each of these ORFs were then analysed using the Codon Use® program (Conrad Halling), which takes into account the codon use frequency in

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N. meningitidis. Only the ORFs with sequences having a maximum frequency of use of these codons were selected. At the end of this analysis, 197 candidate ORFs were selected.

The ORFs selected using this double analysis were subjected to a homology search through all of the available banks, using the BLASTX® program, from the access to the Pathoseq® bank of Incyte Pharmaceuticals. This homology search made it possible to exclude the ORFs encoding, a priori, cytoplasmic or periplasmic proteins, in particular metabolism proteins. The ORFs were also subjected to analysis of possible protein motifs, using the DNA Star Protean® program (Lasergene software).

The authors of the present invention then investigated whether the ORFs selected at the end of the previous step (118 in number) were effectively absent from N. lactamica, as predicted by the application of the prior art WO 98/02547.

To this end, a PCR amplification was carried out. This amplification proved to be ineffective for 78 of the 118 ORFs tested. Only the ORFs for which the amplification in N. lactamica was negative (sequences named "lactamica") were selected. In order to verify that these negative results were not "false negatives", the lactamica sequences selected were subjected to a control by dot blot. At the end of this step, only 23 ORFs were confirmed N. meningitidis /N. lactamica.

Finally, these 23 ORFs were repositioned in their entirety on the $N.\ meningitidis\ {\tt ATCC13090}$ genome. This made it possible to demonstrate that three ORFs previously eliminated on the basis of their putative protein function appeared to be located close to, or of the 23 some framed by, were even These three ORFs N. meningitidis⁺/N. lactamica ORFs. (SEQ ID Nos 29, 35 and 37) were reintroduced into the also proven that they were it was and N. meningitidis+/N. lactamica.

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authors of the present invention then attempted to discover whether the ORFs identified using the genome of the N. meningitidis serogroup B strain the genomes 13090 were also present in N. meningitidis serogroup A Z2491 (Sanger Centre) and of N. gonorrhoeae FA1090 (Advanced Centre of Genome Technology, Oklahoma University). Then, they compared the sequences derived from these various genomes, with multiple alignment (Clustal, Infobiogen). This made it possible to redefine, for some of the ORFs, the most initiation codon position of the probable The sequences of translation stop codon. the open reading frames derived from the strain ATCC13090 are given in the SEQ ID Nos 1-51 (odd numbers) and the amino acid sequences which are deduced therefrom are given in the SEQ ID Nos 2-52 (even numbers).

invention present subject of the therefore, a nucleic acid in isolated form encoding a antigenic fragment polypeptide, or an excluding the nucleic acids disclosed in SEQ ID Nos 70, 73, 74, 77, 80, 81, 87, 88, 89, 94, 95 and 98 of application WO 98/02547 (seguences attached to the present description and numbered SEQ ID Nos 70A, 73A, 74A, 77A, 80A, 81A, 87A, 88A, 89A, 94A, 95A and 98A so to distinguish them from the sequences of said polypeptide having an amino invention); sequence which is identical or homologous to a sequence selected from those of group II; group II consisting of the sequences shown in SEQ ID Nos 2-52 (even numbers) and the sequence SEQ ID No. 53.

Preferably, said nucleic acid can have a nucleotide sequence selected from those of group I, group I consisting of the sequences shown in SEQ ID Nos 1-51 (odd numbers).

The term "nucleic acid" includes and means equally ORF, gene, polynucleotide, DNA and RNA. The term "nucleic acid in isolated form" means a nucleic acid separated from the biological environment in which it is found under natural conditions. For example, a

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DNA molecule exists under natural conditions when it is integrated into a genome or when it forms part of a library of genes. In that case, it cannot be in isolated form. On the other hand, the same molecule separated from the genome by cloning (for example subsequent to a PCR amplification) should be considered as being in isolated form. Typically, a DNA molecule in isolated form does not contain the coding regions which are contiguous with it in 5' and 3' in the genome from which it is derived. The nucleic acids in isolated form can be integrated into vectors (for example plasmids, or viral or bacterial vectors) without, even so, abandoning their characteristic of being separated from their natural environment.

The authors of the present invention have more particularly found that the ORFs which, when they are derived from the strain ATCC 13090, are characterized by the sequences as shown in SEQ ID Nos 19, 27, 39, 45, 47 and 49 are specific for Neisseria meningitidis insofar as it has not been possible to demonstrate identical or homologous sequences in the N. gonorrhoeae genome. They have also found that the ORF characterized by the strain sequence as shown in SEQ ID No. 39 is specific for Neisseria meningitidis serogroup B.

A subject of the invention is also a polypeptide in isolated form, or a fragment thereof; said polypeptide having an amino acid sequence identical or homologous to a sequence selected from those of group II.

The amino acids framed in the sequence SEQ ID No. 8 correspond to the signal sequence, and the amino acid in bold represents the first amino acid of the mature form. The amino acid sequence of the mature protein form is represented in SEQ ID No. 53.

In the context of the present invention, the terms "polypeptide" and "protein" are equivalent and mutually interchangeable. They refer to any amino acid chain, whatever its length and its post-translational

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modifications (for example phosphorylation or glycosylation).

The expression "antigenic fragments polypeptides specific for pathogenic strains of Neisseria genus" is intended to mean the polypeptides derived from the polypeptides of the invention as defined above, through deletions of portions of said polypeptides without destroying the antigenicity (for example, without notable loss of the The specific of said polypeptides. activity) antigenicity can be determined using various methods known to those skilled in the art, as explained later.

These fragments are preferably at least 12 amino acids long, more preferably at least 20 amino acids long, preferentially 50 amino acids long, more preferably still 75 amino acids long, preferentially 100 amino acids long.

These fragments can be used to reveal epitopes which may be masked in the parent polypeptides. They are also advantageous for inducing a T-lymphocytedependent protective immune response. The possible to eliminate fact, make it variable which are highly immunodominant regions between various strains.

Such fragments can be obtained using standard techniques known to those skilled in the art (for example, Ausubel et al., Current Protocols in Molecular Biology, John Wiley & Sons Inc, 1994), for example by PCR, RT-PCR or treatment with restriction enzymes for the cloned DNA molecules, or by the method of Kunkel et al. (Proc. Natl. Acad. Sci. USA (1985) 82:448).

The expression "homologous amino acid sequence" is intended to mean a sequence which differs from one of the sequences of group II by substitution, deletion and/or insertion of one or more amino acids, at positions such that these modifications do not destroy the specific antigenicity of the polypeptide in question.

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Said substitutions are preferably conservative substitutions, i.e. substitutions of amino acids of the same class, such as substitutions of amino acids with uncharged side chains (for instance asparagine, glutamine, serine, threonine and tyrosine), of amino acids with basic side chains (for instance lysine, arginine and histidine), of amino acids with acid side chains (for instance aspartic acid and glutamic acid) or of amino acids with apolar side chains (for instance glycine, alanine, valine, leucine, isoleucine, proline, phenylalanine, methionine, tryptophan and cysteine).

Advantageously, a homologous amino acid sequence has at least a 75% degree of homology (i.e. of identity) with one of the sequences of group preferably this degree of homology is at least 80%, most preferably at least 90%. The homologous amino acid sequences include, in particular, the sequences which are substantially identical to one of the sequences of group II. The expression "substantially identical sequence" means a sequence which has at least a 90%, advantageously at least a 95%, preferably at least a 97%, and most preferably at least a 99%, degree of homology (i.e. of identity) with one of the sequences of group II. In addition, it may differ from the reference sequence only through mainly conservative substitutions.

The degree of homology (also named degree of identity) is generally determined using a sequence analysis program (for example, Sequence Analysis Software Package of the Genetics Computer Group, University of Wisconsin Biotechnology Centre, 1710 University Avenue, Madison, WI 53705). Similar amino acid sequences are aligned so as to obtain the maximum degree of homology (i.e. identity). To this end, it may be necessary to artificially introduce gaps into the sequence. Once optimal alignment has been produced, the degree of homology (i.e. identity) is established by recording all the positions for which the amino acids

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of the two sequences compared are identical, with respect to the total number of positions.

"homologous nucleotide The expression sequences" is intended to mean sequences which differ from the sequences of group I by substitution of one or more nucleotides, or by deletion and/or insertion of more codons, at positions such that these one or sequences (i) still encode polypeptides having the sequences of group II, due to the effect the the genetic degeneracy of code; or (ii) encode polypeptides having homologous sequences defined as above.

Advantageously, a homologous nucleotide sequence has at least a 60% degree of homology with one of the sequences of group I; preferably this degree of homology is at least 80%, most preferably at least 90%.

Typically, a homologous nucleotide hybridizes specifically to the sequences complementary of group I, under sequences conditions. The temperature at which the hybridization assay is carried out constitutes an important factor which influences the stringency. Conventionally, this temperature, termed hybridization temperature (Th), is selected from 5 to 40°C, preferably from 20 to 25°C, below the temperature at which 50% of the paired strands separate (Tm). In general, it is considered that conditions of high stringency are satisfied when Th is lower than Tm by 5 to 25°C approximately, for example by 5 to 10°C or, most commonly, by 20 to 25°C approximately. Moderate stringency is established when Th is lower than Tm by 30 to 40°C.

For sequences comprising more than 30 bases, the temperature Tm is defined by the equation: Tm = 81.5 + 0.41(%G+C) + 16.6Log(cation concentration) - 0.63(%formamide) - (600/number of bases). Thus, ionic strength has a major impact on the value of <math>Tm. The temperature Tm increases by 16.6°C every time the monovalent cation concentration increases by a factor of 10. The addition of formamide into the hybridization

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buffer causes, on the other hand, the value of Tm to decrease. (For a complete reference, see Sambrook et al., Molecular Cloning, A laboratory manual, Cold Spring Harbor Laboratory Press, 1989, pages 9.54-9.62).

Conventionally, hybridization experiments are carried out at a temperature of 60 to 68°C, for example at 65°C. At this temperature, stringent hybridization conditions can, for example, be implemented in 6xSSC, preferably advantageously in 2xSSC or1xSSC, (in the 0.3xSSC or 0.1xSSC absence 0.5xSSC, formamide). A solution of 1xSSC contains 0.15 M of NaCl and 0.015 M of sodium citrate.

For this reason, in other words, a subject of the invention is a polynucleotide in isolated form, which is capable of hybridizing, under stringent conditions, with a DNA molecule having one of the nucleotide sequences as shown in SEQ ID Nos 1-51 (odd numbers) or the sequences complementary thereto.

of homologous class specific consists of those encountered naturally by virtue of 20 the extremely common phenomenon of allelic variation. A species, for example N. meningitidis bacterial N. gonorrhoeae, consists of a large variety of strains which differ from one another through minor variations, termed allelic variations. Thus, a polypeptide which is 25 in various strains and which, of course, performs the same biological function in each of them, can have an amino acid sequence which is not identical from one strain to the other. In other words, the sequences derived from the allelic variation are purely 30 equivalent or alternative to sequences group II. The class of sequences which are allelic variants of one of the sequences of group II consists of the sequences of the polypeptide as found in a pathogenic species of the Neisseria genus (for example, 35 N. gonorrhoeae) other than N. meningitidis or 13090. biological N. meningitidis strain ATCC The function which is associated with the allelic variant sequences is the same as that which is associated with

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the reference sequence. The differences (substitution, deletion or addition of one or more amino acids) which they exhibit between one another (including reference sequence) do not modify the biological function of the polypeptide. The term "biological function" is intended to mean the function exercised by the polypeptide in the cells which produce naturally.

The allelic variation is also expressed in the coding polynucleotide, sequences. Α encoding polypeptide, having a sequence which is an allelic variant of one of the sequences of group I can be easily cloned by amplifying the genomic DNA of the strains of pathogenic species of the Neisseria genus, for example by PCR (polymerase chain reaction), using synthetic oligonucleotide primers capable hybridizing to the 5' and 3' ends of the coding region. The sequences of such primers can easily be established by those skilled in the art using the nucleotide sequences given in SEQ ID Nos 1-51 (odd numbers). primers generally have from 10 to 40 nucleotides, preferably from 15 to 25 nucleotides.

For this reason, in other words, a subject of the invention is a DNA molecule in isolated form which can be amplified and/or cloned by PCR from the genome of a pathogenic Neisseria strain, using a pair of 5' and 3' PCR primers; the sequences of these primers being established using one of the nucleotide sequences as shown in SEQ ID Nos 1-51 (odd numbers). An example is given, for each pair of primers, in Example I.1 hereinafter.

A subject of the present invention is more particularly the allelic variants having the nucleotide sequences SEQ ID Nos 54 to 76 (even numbers) and the products encoded by these nucleotide sequences, having the amino acid sequences SEQ ID Nos 55 to 77 (odd numbers).

The polypeptides of the invention can be fused to other polypeptides, for example by translation of a

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hybrid gene. Vectors for expressing fusion polypeptides are commercially available, such as the vectors pMal-c2 or pMal-p2 from New England Biolabs, in which the protein to which the polypeptides of the invention can be fused is a maltose-binding protein, the glutathione-S-transferase system from Pharmacia or the His-Tag system from Novagen. Such systems are in particular useful for purifying the polypeptides of the invention. The polypeptides of the invention can be fused to polypeptides having adjuvant activity, such as for example the B subunit of cholera toxin or the B subunit of the E. coli heat-sensitive toxin.

The nucleic acids of the present invention can be used (i) in a process for producing the polypeptides encoded by said nucleic acids, in a recombinant host for the construction of vaccination (ii)vectors, such as poxviruses, intended to be used in methods and compositions for preventing and/or for pathogenic Neisseria infection with an treating particular with Neisseria meningitidis, in strains, (iii) as a vaccination agent in a naked form or in combination with a vehicle which promotes transfer to the target cells and, (iv) in the construction of attenuated Neisseria strains which can overexpress a nucleic acid of the invention, or express it in a nontoxic, mutated form.

The present invention also provides (i)expression cassette containing a polynucleotide of the invention placed under the control of elements allowing its expression, in particular under the control of a suitable promoter; (ii) an expression vector containing expression cassette; (iii) а host cell with transformed an eukaryotic) (prokaryotic or expression cassette and/or an expression vector (iv) a method for obtaining a and defined above, polypeptide encoded by said polynucleotide invention, comprising culturing said transformed cell under conditions allowing the expression of the

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polynucleotide of the invention, and recovering the polypeptide from the cell culture.

Among the eukaryotic hosts which can be used, mention may be made in particular of yeast cells (for example Saccharomyces cerevisiae or Pichia Pastoris), mammalian cells (for example COS1, NIH3T3 or JEG3) arthropod cells (for example Spodoptera frugiperda (SF9)) and plant cells. Among the prokaryotic hosts which can be used, mention may be made in particular of E. coli.

The choice of the expression cassette depends system chosen, and also on characteristics desired for the expressed polypeptide. In general, expression cassettes include a promoter which is functional in the host system selected and which can be constitutive or inducible; a ribosomebinding site; an initiation codon (ATG); if necessary, region encoding a signal peptide; a nucleotide stop codon; invention; а the sequence of optionally, a 3' terminal region (translation and/or transcription terminator). The open reading frame (ORF) consisting of the nucleotide sequence of the invention, alone or associated with the region encoding the signal peptide, is placed under the control of the promoter such that translation and transcription take place in the host system. The promoters and regions encoding the signal peptides are known to those skilled in the art. Among them, mention may be made in particular of the (araB promoter) arabinose-inducible promoter Salmonella typhimurium, which is functional in Gram bacteria such as E. coli (US 5,028,530 and Cagnon et Protein Engineering (1991) 4(7): 843), promoter of the T7 bacteriophage gene encoding RNA polymerase (US 4,952,496), and the OspA and RlpB signal peptide (Takase et al., J. Bact. (1987) 169:5692).

The polypeptide expressed can be recovered in a practically purified form from the cell extract or from the supernatant, after centrifuging the recombinant cell culture. The recombinant polypeptide can, in

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particular, be purified using methods of affinity purification with the aid of antibodies, or using any other method known to those skilled in the art, for instance by genetic fusion with a small binding domain.

The nucleic acids of the invention can also be used in the field of vaccination, either by using a viral or bacterial host as a vehicle for releasing the DNA, or by administering the nucleic acid of interest in a free form.

A subject of the present invention is also (i) a vaccination vector containing a nucleic acid of the placed under the control of elements invention, expression; (ii) a pharmaceutical allowing its therapeutically containing a composition prophylactically effective amount of said vaccination vector; (iii) a method for inducing an immune response against Neisseria in a vertebrate, in particular a mammal, preferably a human, said method comprising the administration to said vertebrate of an immunologically effective amount of said vaccination vector so as to cause an immune response, in particular a protective or therapeutic response to Neisseria meningitidis; a method for preventing and/or treating Neisseria strains, infection with pathogenic particular with Neisseria meningitidis, which comprises the administration of a prophylactic or therapeutic amount of said vaccination vector of the invention to an individual requiring such a treatment.

In combination with the polypeptides of the invention, the vaccination vector as defined above can also comprise nucleotide sequences the expression of which allows the immune response to be stimulated, such as the sequences encoding cytokines.

Said vaccination vector of the invention can be administered via any route which is conventional in the field of vaccination, in particular via the parenteral route (for example subcutaneous, intradermal, intramuscular, intravenous or intraperitoneal route). The dose depends on many parameters which are known to

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those skilled in the art, such as the vector itself, the route of administration, or the weight, age or sex of the animal or of the human to be vaccinated.

A subject of the present invention is also (i) composition containing pharmaceutical therapeutically or prophylactically effective amount of a polynucleotide of the invention; (ii) a method for against pathogenic immune response inducing an Neisseria strains, in particular Neisseria meningitidis in a vertebrate, by administering to said vertebrate an immunologically effective amount of said polynucleotide so as to cause an immune response, in particular a protective immune response against pathogenic Neisseria strains, especially Neisseria meningitidis; and (iii) a method for preventing and for treating an infection with pathogenic Neisseria strains, in particular with Neisseria meningitidis, by administering a therapeutic or prophylactic amount of said polynucleotide to an individual requiring such a treatment.

The polynucleotides of the invention (DNA or RNA) can be administered to a vertebrate as they are. When a DNA molecule of the invention is used, it can be in the form of a plasmid incapable of replicating in a vertebrate cell and incapable of integrating the genome of said vertebrate. Said DNA molecule is, typically, placed under the control of a promoter suitable for expression in a vertebrate cell. Said polynucleotide used as vaccine can be formulated according to various methods known to those skilled in the art. polynucleotide can, in particular, be used in a naked form, free of any vehicle which promotes transfer to the target cell, such as anionic liposomes, cationic microparticles, for example gold lipids, example microparticles, precipitation for agents, calcium phosphate, or any other agent which facilitates 35 transfection. In this case, the polynucleotide can be physiologically acceptable a diluted in simply solution, such as a sterile solution or a sterile

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buffer solution, in the presence or absence of a vehicle. When it is present, this vehicle can be preferably isotonic, hypotonic or slightly hypertonic, and has a relatively low ionic strength. It can, for example, be a sucrose solution (for example a solution containing 20% of sucrose).

polynucleotide of Alternatively, a invention can be combined with agents which facilitate transfection. It can be, inter alia, (i) combined with a chemical agent which modifies cell permeability, such (ii) encapsulated (WO 94/16737); bupivacain liposomes, optionally in the presence of additional substances which facilitate transfection (WO 93/18759, WO 93/19768, WO 94/25608 and WO 95/2397, WO 93/18759 and WO 93/19768); or (iii) combined with lipids, or silica, gold or tungsten microparticles.

When the polynucleotides of the invention coat microparticles, these particles can be injected via the intradermal or intraepidermal route, using the "gene gun" technique (US 4,945,050, US No. 5,015,580 and WO 94/24263).

The amount of DNA to be used as a vaccine depends, in particular, on the strength of the promoter used in the DNA construct, on the immunogenicity of the product expressed, on the individual to which this DNA is administered, on the method of administration and on the type of formulation. In general, a therapeutically prophylactically effective amount ranging approximately 1 µg to approximately 1 mg, preferably from approximately 10 μg to approximately 800 μg , and approximately 25 µq from preferentially can be administered to human approximately 250 µg, adults.

invention can be The polynucleotide of the conventional route of via any administered 35 particular via the administration, such as in choice of the route of The route. parenteral particular, the administration depends, in formulation chosen. A polynucleotide formulated

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bupivacain is advantageously with combination administered into muscle. When neutral or anionic DOTMA cationic lipid such as liposomes, ora (N-[1-(2,3-dioleyloxy)propyl]-N,N,N-trimethylammonium (3-beta-(N-(N',N'-dimethyl-DC-Chol or chloride) aminomethane) carbamoyl) cholesterol) used, are formulation can advantageously be injected via the intravenous, intramuscular, intradermal or subcutaneous polynucleotide in а naked form can Α advantageously be administered via the intramuscular, 10

intradermal or subcutaneous route.

The nucleotide sequences of the invention allow the construction of specific nucleotide probes and primers which can be used in diagnosis. Said probes or primers are nucleic acids having sequences identical or homologous to portions of the sequences of group I or to the sequences complementary thereto.

from Preferably, said probes contain approximately 5 to approximately 100, preferably from approximately 10 to approximately 80, nucleotides. They can contain modified bases, the sugar and phosphate residues possibly also being modified or substituted. The probes of the invention can be used in diagnostic tests, to capture or detect polynucleotides specific for pathogenic Neisseria strains. Such capture probes can conventionally be immobilized on a solid support directly or indirectly, by covalent bonding or by passive adsorption. A detection probe can be labelled, in particular with a radioactive isotope, an enzyme such as peroxidase or alkaline phosphatase, or enzymes capable of hydrolyzing a chromogenic, fluorogenic or luminescent substrate, or with compounds which are, themselves, chromogenic, fluorogenic or luminescent, nucleotide analogues; or biotin.

A primer generally contains from approximately 10 to approximately 40 nucleotides, and can be used to initiate enzymatic polymerization of the DNA in an amplification process (for example PCR), in an elongation process or in a reverse transcription

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method. A primer of the invention can in particular be a primer as described in Example II.1 hereinafter.

A subject of the present invention is also:

- (i) a reagent containing a probe of the invention for detecting and/or identifying the presence of pathogenic *Neisseria* strains in a biological sample;
 - (ii) a process for detecting and/or for identifying the presence of pathogenic Neisseria strains in a biological sample, said method comprising the steps consisting in a) extracting the DNA or RNA from a biological sample and denaturing it; b) exposing said DNA or said RNA to a probe of the invention, under stringent hybridization conditions, so as to detect the hybridization; and
- and/or detecting for method (iii) а 15 strains Neisseria pathogenic identifying biological sample, in which the DNA is extracted from a biological sample and mixed together with at least one and preferably with two primers of the invention, and is amplified, for example by PCR. 20

As mentioned above, the polypeptides produced by the expression of the ORF sequences identified can specific agents. The vaccination used as antigenicity of the polypeptides homologous to the sequences of group II polypeptides having evaluated by assaying the cross-reactivity with an having directed against the polypeptides antiserum A monospecific hyperimmune group II. of sequences purified against а produced be antiserum can polypeptide having a sequence of group II or a fusion polypeptide, for example an expression product of the MBP, GST or His-tag systems.

The specific antigenicity can be determined using various methods known to those skilled in the art, in particular the Western blot, dot blot and ELISA techniques, described below.

In the Western blot technique, the protein preparation to be tested is subjected to SDS-PAGE gel electrophoresis. After transfer onto a nitrocellulose

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membrane, the material is incubated with a monospecific hyperimmune antiserum obtained after having immunized an animal with the referent material; i.e., in the present case, with a polypeptide having an amino acid This antiserum is group II. sequence of beforehand in a dilution range of approximately 1:50 to 1:5000, preferably of approximately 1:100 to 1:500. The band is revealed when а antigenicity specific corresponding to the product shows reactivity with one of the dilutions above.

assay, a purified In the ELISA preparation is preferably used, although a whole cell extract may also be used. Approximately 100 μl of a preparation at approximately 10 $\mu g/ml$ are distributed into the wells of a plate. The plate is incubated for two hours at 37°C, and then overnight at 4°C. The plate then washed with a phosphate buffered saline solution (PBS) comprising 0.05% of Tween 20. The wells are saturated with 250 μl of PBS containing 1% of bovine serum albumin (BSA) so as to prevent nonspecific antibody binding. After incubation for one hour at 37°C, the plate is washed with the PBS/Tween buffer. The antiserum is serially diluted in PBS/Tween buffer containing 0.5% BSA. 100 μl of this dilution are added per well. The plate is incubated for 90 minutes at 37°C, washed and evaluated according to standard procedures. For example, when specific antibodies are produced in rabbits, a goat anti-rabbit peroxidase conjugate is added to the wells. The incubation is carried out for 90 minutes at 37°C and the plate is then washed. The reaction is measured by colorimetry (the reaction is positive when the optical density the dilution is at least is 1, if value preferably at least 1:500).

In the dot blot assay, a purified protein is preferably used, it being understood that it is also possible to use a whole cell extract. Two-fold serial dilutions of a protein solution at approximately 100 $\mu g/ml$ are prepared in a 50 mM Tris-HCl buffer,

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pH: 7.5. 100 μ l of each dilution are applied to a nitrocellulose membrane (BioRad apparatus). The buffer is removed by applying suction to the system. The wells are washed by adding 50 mM of Tris-HCl buffer (pH: 7.5) and the membrane is air-dried. The membrane is then blocking buffer (50 mM Tris-HCl in a saturated (pH: 7.5) 0.15 M NaCl, 10 g/l of skimmed milk) incubated with a dilution of antiserum ranging from preferably 1:5000, approximately 1:50 to is revealed The reaction 1:500. approximately accordance with standard procedures. For example, when specific antibodies are produced in rabbits, a goat anti-rabbit peroxidase conjugate is added to the wells. The incubation is carried out for 90 minutes at 37°C. The reaction is developed with the suitable substrate and measured, for example by colorimetry, appearance of a coloured spot (a reaction is positive when a coloured spot appears in association with a dilution of at least 1:50, preferably of at least 1:500).

A subject of the present invention is also (i) composition containing pharmaceutical therapeutically or prophylactically effective amount of a polypeptide of the invention; (ii) a method for pathogenic response against inducing immune an Neisseria strains in a vertebrate, by administering to said vertebrate an immunogenically effective amount of a polypeptide of the invention so as to cause an immune response, in particular a protective immune response against pathogenic Neisseria strains; and method for preventing and/or for treating an infection with pathogenic Neisseria strains, by administering a therapeutic or prophylactic amount of a polypeptide of invention to an individual requiring such a the treatment.

The immunogenic compositions of the invention can be administered via any route which is conventional in the field of vaccination, in particular via the parenteral route (for example subcutaneous,

intradermal, intramuscular, intravenous orintraperitoneal The choice of route). the route of administration depends on certain a number of parameters, such as the adjuvant combined with polypeptide.

A composition of the invention contains at least one polypeptide as defined above. It can also contain at least one additional antigen of Neisseria meningitidis and/or Neisseria gonorrhoeae.

The polypeptides of the invention can be formulated with liposomes, preferably neutral or anionic liposomes, microspheres, ISCOMS or "virus-like" particles, in order to facilitate the transfer of the polypeptide and/or to increase the immune response.

The administration can be carried out with a single dose or with doses repeated, if necessary, at intervals which can be determined by those skilled in the art.

For example, an initial dose can be followed by three booster doses at intervals of one or more weeks 20 or of one or more months. The suitable dose depends on many parameters, including the individual (adult or child), the specific vaccination antigen, the route ΩĒ administration and the frequency 25 administration, the presence or absence or the type of effect adjuvant, and the desired (for protection and/or treatment), and can be determined by those skilled - in the art. Ιf the route of. administration is parenteral, the dose 30 preferentially less than 1 mg, preferably approximately 100 µg. The polypeptides and polynucleotides of the invention used as vaccination agents can be used sequentially, in a several-step immunization process. For example, a vertebrate can be initially sensitized with a vaccination vector of the invention, such as a 35 poxvirus, for example via the parenteral route, and can then be stimulated twice with the polypeptide encoded by the vaccination vector.

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A polypeptide of the invention can also be useful as a diagnostic agent for detecting the presence of anti-Neisseria meningitidis and/or anti-Neisseria gonorrhoeae antibodies in a biological sample such as a blood sample.

A subject of the present invention is also monospecific antibodies directed against the polypeptides of the invention.

The term "monospecific antibodies" is intended to mean an antibody capable of reacting specifically with a Neisseria polypeptide of the invention. Such antibodies can be polyclonal or monoclonal, and can be recombinant antibodies, for example chimeric (for example consisting of a variable region of murine origin associated with a constant region of human origin), humanized and/or single-chain antibodies. Said antibodies can also be in the form of immunoglobulin fragments, for example F(ab)'2 or Fab fragments. The antibodies of the invention can be of any isotype, for example IgA or IgG, the polyclonal antibodies possibly being of a single isotype or possibly containing a mixture of several isotypes.

the invention antibodies of The against the polypeptides of the invention can be produced and identified using standard immunological methods, for example Western blot analysis, a dot blot assay, an ELISA assay (Coligan et al., Protocols in Immunology (1994) John Wiley & Sons, Inc., Said antibodies can be used York. NY). diagnostic processes for detecting the presence of a Neisseria meningitidis antigen in a sample such as, in particular, a biological sample (for example a blood sample).

The antibodies of the invention can also be used in affinity chromatography processes for purifying 35 invention. Finally, such of the polypeptide in prophylactic used antibodies can also be therapeutic passive immunization methods.

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A subject of the present invention is also a diagnostic method for detecting the presence of pathogenic Neisseria strains in a biological sample, comprising bringing said biological sample into contact with an antibody or a polypeptide of the invention, such that an immune complex is formed, and detecting indicates pathogenic Neisseria said complex which strains in the organism from which the originates. Those skilled in the art understand that the immune complex is formed between a component of the sample and the antibody or the polypeptide of the any substance not bound possibly being invention, eliminated prior to the detection of the complex.

Thus, a reagent of polypeptide type can be used for detecting the presence of anti-Neisseria meningitidis and/or Neisseria gonorrhoeae antibodies in a sample, whereas an antibody of the invention can be used as a reagent for assaying the presence of a Neisseria meningitidis and/or Neisseria gonorrhoeae polypeptide in a sample.

For use in diagnostic applications, the reagent (for example the antibody or the polypeptide of the invention) can be in the free state or immobilized on a solid support, by direct or indirect means.

The direct means include passive adsorption or covalent bonding between the support and the reagent.

The term "indirect means" is intended to mean that a substance which interacts with said reagent is attached to the solid support. For example, if a reagent of polypeptide type is used, an antibody which binds to this polypeptide can be used as an antireagent substance, it being understood that this substance binds to an antibody which is not involved in recognizing the antibodies in the biological samples.

Among the indirect means which can be used, mention may also be made of the ligand receptor system, a molecule such as a vitamin possibly being grafted onto the reagent of polypeptide type, and the corresponding receptor possibly being immobilized on

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the solid phase. This is illustrated by the biotinstreptavidin system. It is also possible to add a peptide tail to the reagent, by chemical engineering or genetic engineering, and to immobilize the grafted or fused product by passive adsorption or covalent bonding with the peptide tail.

A subject of the present invention is also a process for purifying, from a biological sample, a Neisseria polypeptide of the invention, by affinity chromatography with a monospecific antibody of the invention. Said antibody is preferably of isotype IgG.

According to an example of implementation, a biological sample, preferably in a buffer solution, is a chromatographic material, preferably applied to equilibrated with the buffer used to dilute biological sample, such that the polypeptide of the may adsorb antigen) invention (i.e. the material. The unbound components are washed and the antigen is then eluted with a suitable elution buffer, such as a glycine buffer or a buffer containing chaotropic agent, for example guanidine HCl, or a high concentration of salt (for example 3 M MgCl₂). eluted fractions are recovered and the presence of antigen is detected, for example by measuring the absorbence at 280 nm.

A subject of the present invention is also (i) a pharmaceutical composition containing a therapeutically or prophylactically effective amount of a monospecific antibody of the invention; and (ii) a method for preventing and/or for treating an infection with pathogenic Neisseria strains, by administering a therapeutic or prophylactic amount of a monospecific antibody of the invention to an individual requiring such a treatment.

To this end, the monospecific antibody of the invention is preferably of isotope IgG, and preferably fixes the complement. Said monospecific antibody according to the invention can be administered alone or in a mixture with at least one other monospecific

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antibody, specific for a different Neisseria meningitidis and/or Neisseria gonorrhoeae polypeptide, according to the invention. The amount of antibody can be determined easily by those skilled in the art. For example, a daily administration of approximately 100 to 1000 mg of antibodies over a week, or three daily doses of approximately 100 to 1000 mg of antibodies over two or three days, may be an effective dose.

The therapeutic or prophylactic effectiveness may be evaluated using standard methods known to those skilled in the art, for example by measuring the induction of an immune response or the induction of protective and/or therapeutic immunity (in newborn rats or mice), through evaluation of the bacterial load in cerebrospinal fluid. The protection can determined by comparing the degree Neisseria of infection to control group. Protection а demonstrated when the infection is decreased comparison with the control group. Such an evaluation be carried out with the polynucleotides, vaccination vectors, the polypeptides and also antibodies according to the invention. The therapeutic or prophylactic effectiveness of a product according to the invention (polynucleotide or polypeptide) can also be evaluated in an assay for bactericidal activity, as described by Danve et al., Vaccine (1993) 11(12):1214 against the meningococcal strain of origin of the polynucleotide or polypeptide used. In the field of meningococcal vaccines, the bactericidal activity assay is, in fact, recognized as being the reference assay based upon which it is possible to make a valid prediction of the vaccination value of a product. product according to the invention is Briefly, a administered to animals such as rabbits in order to produce an antiserum against this product. Then, this antiserum is assayed for its lysis capacity. The bactericidal titre of an antiserum represents the inverse of the dilution of this antiserum for which 50% of the load of meningococci is lysed. The antiserum is

considered to be bactericidal when the titre is higher than 4, with respect to the menigococcal strain of origin of the polynucleotide or polypeptide used. In that case, the product against which the antiserum was generated is demonstrated to be potentially advantageous from a pharmaceutical point of view.

The following examples illustrate the invention without limiting the scope thereof.

10 Legend of the figure

The attached figure represents the vector pCAMyc-His used as a cloning vector.

Details of the strategy for identifying the

15 **ORFs:**

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In order to select the ORF sequences specific for the pathogenic strains of the Neisseria genus, a PCR amplification is carried out on the sequences of the 118 ORFs selected after analysis with the Gene Jockey®, Codon Use®, and homology search programs. Only the sequences for which the amplification in N. lactamica is negative (sequences named "lactamica") are selected. In order to verify that these negative results are not "false negatives", the lactamica sequences selected are subjected to a dot blot.

A - PCR amplification:

A.1. Extraction of genomic DNAs:

genomic DNAs of all of the Neisseria The strains used in this study were prepared according to N.meningitidis, protocol. The identical an subflava and N. mucosa N. lactamica, N. flava, N. strains were cultured on tissues of MHA (Muller Hinton and the N. gonorrhoeae were Difco) medium, cultured on tissues of MHA medium supplemented with 10% of heat-treated horse blood (Biomérieux) and 1% of Isovitalex (Biomérieux). The culturing is carried containing 10% atmosphere under an out

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 CO_2 , overnight at 37°C. Then, the cells are harvested, and washed in PBS phosphate buffer (pH 7.2), and the DNA is extracted according to protocol D of the "Rapid Prep genomic DNA isolation kit for cells and tissue" (Pharmacia Biotech).

The genomic DNAs were then controlled on agarose gel for their completeness and by PCR reaction for their purity.

A.2. PCR reaction for screening the ORFs absent in N. lactamica 2314:

A PCR amplification was carried out on the genomic DNAs of the N. meningitidis strain ATCC 13090 and N. lactamica strain 2314 (ATCC 23970), according to the following protocol:

The PCR reaction was carried out on a 50 μ l volume with 10 ng of genomic DNA, 250 μ M of each of the dNTPs, 300 nM of each of the primers, 1X Taq DNA polymerase buffer and 2 u of Taq DNA polymerase (Appligène).

The amplification cycles are:

	97°C	45 seconds	25	cycles
25	56°C	1 minute	25	cycles
	72°C	2.30 minutes	25	cycles

For each of the ORFs analysed, positive and negative controls for the PCR reaction were carried out. At this stage, only the N. meningitidis+ and N. lactamica- ORFs are selected.

B - <u>Selection of the N. meningitidis</u>* N. lactamica ORFs by dot blot on genomic DNA:

The absence of a product of PCR amplification of an ORF with genomic DNA of N. lactamica 2314 as the matrix does not guarantee the absence of this ORF in the N. lactamica 2314 genome. Specifically, a certain variability in the region to which the oligonucleotides

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should hybridize may be responsible for the absence of amplified product for a given ORF.

context, further verification is this carried out by dot blot on genomic DNA, using, probe, the products of genomic amplification on the N. meningitidis strain corresponding to each of reading frames identified. The dot blot filters contain genomic DNA of the following strains: 2 N. lactamica strains 8064 and 2314, one N. flava strain ATCC 30008, one N. mucosa strain ATCC 9297, 3 N. meningitidis serogroup B strains ATCC13090, M982 and B16B6, strain Z2491, one N. meningitidis serogroup Α N. meningitidis serogroup C strain (strain Z4182) and 2 N. gonorrhoeae strains MS11 and FA1090. This dot blot analysis makes it possible to validate the absence of the ORF in N. lactamica 2314 and 8064, and it is also an indication of the degree of variability of an ORF within the Neisseria strains.

The dot blot technique used is as follows.

20 Approximately 50 ng of genomic DNA, denatured for 5 min at 100°C, of the various Neisseria strains are loaded, with suction, onto a Hybond N+ nitrocellulose membrane (Amersham) placed between the jaws of a dot blot apparatus (BioRad). Then, the DNA is fixed on the membranes for 5 min with UV radiation at 315 nm.

The membranes are incubated in a prehybridization buffer (containing denatured salmon sperm DNA). They are then hybridized with a probe corresponding to the product of amplification of the ORF of interest, labelled according to a cold labelling protocol, such as the "DIG DNA labelling and detection kit" system (Boehringer Mannheim).

The ORF which does not hybridize to the genomic DNA of $N.\ lactamica$ 2314 and 8064 is definitively selected as a potential vaccination candidate.

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Example I: Cloning

1. PCR amplification

Each of the ORFs was amplified by PCR using the genomic DNA of N. meningitidis serogroup B (strain ATCC 13090), according to standard protocol.

Two oligonucleotides, primers on the N-terminal side and on the C-terminal side were defined for each of the ORF sequences of the invention.

The primer on the N-terminal side comprises an enzyme restriction site for cloning, a CCACC Kozak sequence for translation initiation (M. Kozak, J. Mol. Biol. 196: 947-950), the ATG of the potential ORF and approximately 17 bases specific for the 5' portion of the ORF.

The primer on the C-terminal side was defined such that the ORF cloned is in fusion, in its 3' portion, with a repeat of 8 histidines and a stop codon which are present in the vector behind the multiple cloning site, hence the insertion of an "A" base in order to keep the correct reading frame after cloning and the disappearance of the stop codon of the ORF. The primer on the C-terminal side thus comprises an enzyme restriction site for cloning, an "A" base, and then approximately 20 bases specific for the 3' portion of the gene starting from the codon preceding the stop codon.

After searching for restriction sites which are absent in each of the ORFs, with the aid of the DNASTAR MapDraw subprogram (Lasergene Software), the XbaI restriction site in 5' and BglII restriction site in 3' are used for the ORF SEQ ID No. 19. For the ORF SEQ ID No. 41, the SpeI site in 5' and the BglII site in 3' are used. The XbaI restriction site in 5' and BamHI restriction site in 3' are used to clone the remaining ORFs.

The PCR mixture comprises, for a final volume of 100 $\mu l\,,$ 10-50 ng of genomic DNA, the N-terminal and

C-terminal primers each at 200 nM, the dNTPs each at 250 μ M, the 1X PCR buffer (composition of the 10X PCR buffer: 200 mM Tris-HCl (pH 8.8), 20 mM MgSO₄, 100 mM KCl, 100 mM (NH₄)₂SO₄, 1% TritonX-100 and 1 mg/ml of nuclease-free bovine serum albumin) and 2.5 U of polymerase.

The amplification is carried out as follows:

Step	Temperature (°C)	Time (min.)	Number of
			cycles
Denaturation	97	0.45	25
Hybridization	cf. table	1	25
Elongation	72	1/kb DNA	25

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The primers used and the PCR conditions given in the table below, in which "N. g allelic variant" means that an allelic variant is present in Neisseria gonorrhoeae and "N. m A allelic variant" means that an allelic variant is present in Neisseria meningitidis serogroup A.

ORF No.	SEQ ID No.	5' Primer	3' Primer	Polymerase	Hybridization
(internal) H
ref.)			Old You how our		3
22	1-2	GCT CTA GAC CAC CAT GTC TGA AUA	CGG GAT CCA GAA ATG GCT GGA TTC GCT ATC AG (SEQID n° 79)	Tfu	2,95
	N.g allelic variant:			(Appligene)	
	54, 55		COBOCO		
41	3-4	GCT CTA GAC CAC CAT GAA ACA CTT	CGG GAT CCA ATA CGT AGG ACT 1GG	Tfu	43°C
 	1	ACT CAT CG (SEQ ID n° 80)	GTC (SEQ ID n° 81)	(Appligene)	
		THE AND AND CAN CAN AND AND AND AND AND AND AND AND AND A	COG GAT CCA TTG CGG ATA AAC ATA	T1.£1.1	יסאנ
42-43	5-6	GCI CIA (IAC CAL CAI UAA AAA AAC	TTC CCIC C (SEO ID nº 83)	7 7 7))
	N.g allelic variant:	(26 11 (27) 21 (27) 1 (27) 1 (27)		(Appligene)	
	י אח				
	70,00	010000000000000000000000000000000000000	CONTRACTOR GIVE GITA GCC TAC	, i	7071
47	7-8	GCT CTA GAC CAC CAT GCG AAC GAC	GGG GAT CCA GAA CCG GTA GGC TTG GCC GAC (SEQ ID nº 85)	na.r.	ر د د
	N.g allelic variant:			(Appligene)	
	58, 59		000 00 00 00 00 00 00 00 00 00 00 00 00		
55	9-10	GCT CFA GAC CAC CAT GAA CAC ACG	CGG GAT CCA GCA ACG GCC 1915 CGC TITE C	Pfu Turbo	26°C
	N.g allelic variant:	CALCALCAL TO (SEATER CO.)		(Stratagene)	
	60, 61				
89	21.17	GCT CTA GAC CAC CAT GCT GAC GTT	CGG GAT CCA CGG CAG AGG CAC GAT	Tfu	2e,C
) 	1	TAT CGG ACT G (SEQ ID n° 88)	TCC (SEQ 1D II 99)	(Appligene)	

				operom: Log	Hybridization
ORF No.	SEQ ID No.	5' Primer	3' Primer		Ë
(internal					
ref.)		CONTRACTOR CARGO AND ANA CHE	COS CATTOCA CITA OCT GOG CAG CIT	Df.1 Tirbo	2,95
105	27-28	GCF CTA GAC CAC CAT GCA AAA CAG	COUNTY CON DIACON CONTRACTOR	, , , , , , , , , , , , , , , , , , , ,	
) 1 1		(UCA ATC (SEQ ID II 197)	(Stratagene)	
		GCT CTA GAC CAC CAT GAC ATT GCT	CGG GA'F CCA TTC CGC AAA TAC CTG	Tfu	26°C
128	29-30	CAA TCT AAT GAT AAT G (SFQ ID nº 106)	TIT CCA ACC (SEQ ID nº 107)	(Appliaene)	
	N.mA. allelic				
	variant: 68, 69		ACK ACK TAC TTO GGC GCA ACA	Acres March	7075
152	31-32	GCT CTA GAC CAC CAT GAA ACA ATC	CGG GAT CLA 1AC 11G GGC GGS 11G1	PIU IUINO)
1	N ~ 2] C C N = 173 x ant .	500 - 500 500 500 500 500 500 500 500 50		(Stratagene)	
	N.9 allello varianici				
	70, 71	1 LLAN TO COMPANY	CONTRACTOR TIME THAT AGA COT ATTENT	44.1.	2600
	70 00	GCT CTA GAC CAC CAT GAA TGT TIA	CGG GAT CCA 111 111 AGA CG1 A11 111	ntt)
153	35 - 54	CGG T11 CCC (SFQ ID nº 110)	AGT CG (SEQ ION 111)	(Appligene)	
		ACT CTA GAC CAC CAT GAT GAG TCA	CGG GAT CCA TCC AGT TIT TGC TCG	Tfu	2e°C
155	35-36	ACA CTC IGC C (SEQ ID nº 112)	AAG GC (SEQ ID n° 113)	(Appligene)	
	1 1	GCT CTA GAC CAC CAT GCC 1TC GAG	CGG GAT CCA TCG TTC TTC AAT CTC CAC	Tfu	26°C
156	37-38	CAA AAA CTG G (SEQ ID nº 114)	AAA CG (SEQ 1D nº 115)	(Appligene)	
		GCT CTA GAC CAC CAT GCA CC	GET C'TA GAC C'AC CA'F GCA CCT CGG GAT CCA TIC AAT TCG CTT CAA	Tfu	2e,g
157	39-40	TGG AAA G (SEQ ID n° 116)	CAA TG (SEQ ID n° 117)	(Appligene)	

ON FIGO	NO UE CER	5' Primer	3' Primer	Polymerase	Hybridization
(internal					° H
ref.)			OLD CAR HAR STORES		
158	41-42	GGA CTA G1C CAC CAT GCC 1GC CAA CCA ACG 1TA CCG (SEQ ID nº 118)	GAA GAT CTA AGC CGC GTT CCC LTC CAA AAA ATC (SEQ ID nº 119)	Tfu	2°95
	N.mA. allelic			(Appligene)	
	variant: 72, 73		COC Sine City		
159	43-44	GCFCTA GAC CAC CAT GCC GCA AAT TAA AAT TCC C (SEQ ID n° 120)	CGG GAT CCA AAA ACA ATC 11C CGG CAC CC (SEQ ID n° 121)	rfu	26°C
	N.mA. allelic			(Appligene)	
	variant: 74, 75				
171	75-76	GCT CTA GAC CAU CAT GCG CAC GCC	CGG GAT CCA TTG GGC AAC GAC GAA	Tfu	26°C
1 0 1) H	GTT 'I'IG (SEQ ID n° 122)	GGC AC (SEQ ID n° 123)	(Appligene)	
7 ()	77 - 40	GCT CTA GAC CAC CAT GAG AAT	CGG GAT CCA TGG CTC AAT CCT TTC TGC	Pfu Turbo	2,95
T : C O T	O # - / #	AGA GAT CAC ACC (SEQ ID nº 124)	(SEQ ID n° 125)	(Stratagene)	
7	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	GCT CTA GAC CAC CAT GAT TCA CGT	CGG GAT CCA ACC TGC TTC ATG GGT	Tfu	2°95
7-50T	つ つ い ・	TFC GGC AGT G (SEQ ID n° 126)	GATTC (SEQ ID n° 127)	(Appligene)	
167_168	27-L7	GCT CTA GAC CAC CAT GAA TIC GAC	CGG GAT CCA AAT CCC TCT GCC GTA	Tfu	26°C
001-/01	10	CGC AAG TAA AAC (SEQ ID nº 128)	TTT G (SEQ ID n° 129)	(Ann i gene)	
	N.gallelic variant:			(ついろですづけ)	
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2- Cloning, transformation and selection of recombinants

The cloning vector used is the 6.357 kb vector. pCA/Myc-His or pM1070 (cf. figure), derived from the plasmid pCDNA 3.1 (Invitrogen). pCA/Myc-His comprises, in particular, the CMV iel promoter (bases 249-902), intron A of the CMV iel gene (Chapman et al., 19, 3979-3986), a multiple Nucleic Acids Research, cloning site (bases 1792-1852) with the PmlI, EcoRV, NotI, XbaI, BamHI, KpnI and HindIII sites, a sequence encoding a polyhistidine and a stop codon termination 1908-1928), a bgh 3′ sequence 1853-2197) and the ampicillin resistance gene selecting the recombinant clones in E. coli.

After purification (GeneClean Bio101 kit), the PCR amplification products are digested for 2 hours at 37°C with the appropriate enzymes (XbaI-BamHI, XbaI-BqlII or SpeI-BqlII), in a final reaction volume of $20 \mu l$. The digestion products are then ligated with the vector pCA/Myc-His, digested beforehand with XbaI and BamHI, according to the "Rapid DNA Ligation Kit" protocol (Boehringer Mannheim). 15 µl of the ligation is used to transform 100 μl of competent E. coli XLIblue cells (Novagen). The cells are incubated for 30 minutes in ice, 30 seconds at 42°C and 2 minutes in ice. Then, 500 μl of LB medium without antibiotics are added, and the mixture is incubated for 1 hour at 37°C. Next, 50 and 550 μ l of the culture are plated out on plates containing LB medium plus ampicillin (50 μ g/ml final concentration), and incubated overnight at 37°C.

The following day, 36 colonies are placed in culture in 2 ml of LB plus ampicillin (50 $\mu g/ml$) and incubated overnight at 37°C.

The following day, the plasmid DNA is extracted according to the Qiagen mini-prep protocol (Qiagen) and the recombinants are identified by enzymatic restriction followed by agarose gel electrophoresis. The cloning junctions are then verified by sequencing.

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Example II: Evaluation of the protective activity of the ORFs of the invention

Preparation of the DNA intended for the immunization experiments: 5

An isolated colony of a recombinant clone is medium preculture in LB inoculate a ampicillin, and 5 ml of this preculture represents the inoculum of a 2.5 litre culture in LB medium + ampicillin. The purification protocol for preparing the plasmid DNA is that described in the EndoFree Giga Kit is eluted from DNA purified (Qiagen). The purification column with a 10 mM Tris-HCl, 1 mM EDTA buffer, pH 8, and stored at -20°C. Before injection, diluted recombinant plasmid is purified injectable preparation (of water with 100 µg/ml quality) and the NaCl concentration is brought to 150 mM.

Production of a specific polyclonal в. serum:

Hyperimmunization in an animal model:

The animal model used is the mouse or the rabbit. The route of administration of the injected DNA intradermal or route. the intramuscular recombinant plasmids to be injected are optionally applied to beads if they are injected into animals using a gene gun apparatus (BioRad). The immunization 30 protocol follows a scheme comprising two injections, 3 weeks apart.

Analysis of the bactericidal activity of the antibodies induced: 35

Ten days after the final injection, the animals are analysed using sera the bactericidal activity assay according to the protocol of Danve et al., Vaccine (1993) 11 (12):1214. Briefly,

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the sera are incubated at various dilutions (2-fold) in the presence of rabbit complement and of meningococci cultured in the presence or absence of an ironchelating agent. The bactericidal titre of a serum represents the inverse of the dilution of this antiserum for which 50% of the bacteria are lysed.

It is considered that the antiserum is not bactericidal when its titre is lower than 4 against the homologous strain.

When the bactericidal titre corresponds to a 4-fold seroconversion against the homologous strain, the bactericidal activity of the antiserum is analysed against other *Neisseria* strains in order to measure the extent of the cross-reactivity of the antiserum of interest.

Example III: Production of purified recombinant proteins

1. Recombinant production of proteins

a. Preparation of transformants:

The PCR product obtained is then digested at $37\,^{\circ}\text{C}$ for two hours with restriction enzymes, in 20 μl of reaction volume. The digestion product is ligated into a plasmid pET28a (Novagen) which is cleaved in a similar way and which is dephosphorylated, before ligation, by treating with calf intestine alkaline phosphatase. The fusion gene constructed in this way allows the one-step affinity purification of the resulting fusion protein, due to the presence of histidine residues at the N-terminal end of the fusion protein, which are encoded by this vector.

The ligation reaction (20 μ l) is carried out at 14°C overnight, before transforming 100 μ l of fresh competent *E. coli* XL1-blue cells (Novagen). The cells are incubated on ice for two hours, and then subjected to a heat shock at 42°C for 30 seconds, before being returned to the ice for 90 seconds. The samples are

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then added to 1 ml of LB broth without selection, and cultured at 37°C for two hours. The cells are then plated out on LB agar medium supplemented with kanamycin (50 μ g/ml final concentration) at a 10× dilution, and are incubated overnight at 37°C. The following day, 50 colonies are subcultured on secondary plates and are incubated at 37°C overnight.

b. Production of the protein:

The stored transformants (10 μ l) are plated out onto selection plates and cultured overnight at 37°C. A few cells are harvested from the plate and used as an inoculum for an overnight starter culture (3 ml) at 37°C . The following day, a sample (time T = 0) is taken and centrifuged at 14 000 rpm for 3 minutes. starter culture is then used to inoculate an LB medium containing kanamycin (100 $\mu g/ml$) at a dilution of 1:50 (starting optical density $OD_{600} = 0.05-0.1$). The cells are cultured to an OD_{600} of 1.0, a sample is taken for the (pre-induction sample) and SDS-PAGE culture is induced with 1 mM of IPTG. The cultures are cultured for four hours and samples are taken every centrifuged 600 q at is culture hour. The 20 minutes at 4°C. The supernatant is discarded and the pellets are resuspended in 50 mM of Tris-HCl (pH: 8.0), EDTA, and recentrifuged. The supernatant is discarded and the cells are stored at -70°C.

2. Protein purification

The pellets obtained from one litre of culture prepared according to Example I.4 above are dried and resuspended in 20 ml of 20 mM Tris-HCl (pH 8.0), 0.5 M NaCl, 5 mM imidazole, cooled in ice. Lysozyme is added at a concentration of 0.1 mg/ml, and the suspension is homogenized using a high-speed homogenizer (Turrax), then treated with a sonicator (Sonifier 450, Branson). Benzonase (Merck) is used at a final concentration of 1 U/ml in order to eliminate the DNA. The suspension is centrifuged at 40 000 g for 20 minutes and the

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supernatant is filtered through a 0.45 µm membrane. The supernatant is loaded onto an IMAC column (12 ml of resin) which has been prepared by immobilizing Ni⁺⁺ cations according to the manufacturer's recommendations (Pharmacia). The column is washed with 10 column volumes of 20 mM Tris-HCl (pH 8.0), 0.5 M NaCl, 60 mM imidazole. The recombinant protein is eluted with six volumes of 20 mM Tris-HCl (pH: 7.9), 0.5 M NaCl, 500 mM imidazole, 0.1% Zwittergent 3-14.

The elution profile is controlled by measuring the absorbence of the fractions at an optical density 280 nm. An aliquot fraction is analysed on an SDS-PAGE gel and stained with Coomassie blue (Phast System - Pharmacia), and the fractions corresponding to the protein peak are then pooled and concentrated. In order to eliminate the elution buffer, the fraction is passed over a G24 Sephadex column (Pharmacia) and equilibrated in PBS buffer (pH: 7.4). The protein solution is sterilized by filtration through a 0.45 μm membrane, and the protein concentration is determined the BCA micromethod (Pierce). The protein solution is stored at -70°C.

Example IV: Production of monospecific polyclonal antibodies

1. Rabbit hyperimmune antiserum

100 μg (in total) of the polypeptide purified in Example III, in the presence of complete Freund's adjuvant in a total volume of approximately 2 ml, are injected into New Zealand rabbits, both subcutaneously and intravenously. 21 and 42 days after the initial injection, the booster doses, which are identical to the initial doses, are administered in the same way, with the exception that incomplete Freund's adjuvant is used. 15 days after the final injection, the animal's serum is recovered, decomplemented and filtered through a 0.45 μ m membrane.

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2. Mouse hyperimmune ascites fluid

 $10-50 \mu g$ of the purified fusion polypeptide obtained in Example II, in the presence of complete Freund's adjuvant, in a volume of approximately 200 μ l, are injected subcutaneously into 10 mice. 7 and 14 days after the initial injection, booster doses, which are identical to the initial doses, are administered in the same way, with the exception that incomplete Freund's adjuvant is used. 21 and 28 days after the initial injection, the mice receive 50 μg of the antigen alone, intraperitoneally. On the 21st day, the mice are also injected intraperitoneally with 180/TG CM26684 sarcoma cells (Lennette & Schmidt, Diagnostic procedures for viral, rickettsial, and chlamydial infections, (1979) Public Health Washington DC, American 5th Ed. Association). The ascites fluids are harvested 10 to 13 days after the first injection.

Example V: Purification of the polypeptides of the invention by immmunoaffinity

Purification of specific IgG

An immune serum as prepared in Example IV is applied to a Fast Flow Sepharose 4 protein A column (Pharmacia) equilibrated with 100 mM Tris-HCl (pH: 8.0). The resin is washed by applying 10 column volumes of 100 mM Tris-HCl and 10 volumes of 10 mM Tris-HCl (pH: 8.0) to the column. The IgGs are eluted with a 0.1 M glycine buffer (pH: 3.0) and are collected by 5 ml fraction, to which 0.25 ml of 1 M Tris-HCl (pH: 8.0) are added. The optical density of the eluate is measured at 280 nm and the fractions containing the IgGs are pooled and, if necessary, stored at -70°C.

2. Column preparation

A suitable amount of CNBr-activated Sepharose 4B gel (1 g of dried gel providing approximately 3.5 ml of hydrated gel, and the capacity of the gel ranging from 5 to 10 mg of coupled IgG per ml of gel)

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manufactured by Pharmacia (17-0430-01) is suspended in 1 mM HCl buffer and washed, using a Buchner funnel, by adding small amounts of 1 mM HCl buffer. The total volume of the buffer is 200 ml per gram of gel.

The purified IgGs are dialysed for four hours at 20 \pm 5°C against 5 volumes of 500 mM PBS buffer (pH: 7.5). Then, they are diluted in 500 mM of PBS (pH: 7.5) for a final concentration of 3 mg/ml.

The IgGs are incubated with the gel overnight at 5 ± 3°C, with stirring. The gel is packed into a chromatography column and washed with 2 column volumes of 500 mM phosphate buffer (pH: 7.5) and then one volume of 50 mM NaCl sodium buffer (pH: 7.5). The gel is then transferred to a tube, then incubated with 100 mM of ethanolamine (pH: 7.5) for 4 hours at room temperature with stirring, and then washed twice with two column volumes of PBS. The gel is then stored in PBS merthiolate at 1/10 000. The amount of IgG coupled to the gel is determined by measuring the optical density at 280 nm of the IgG solution and of the direct eluate.

Adsorption and elution of the antigen

Tris-HCl solution of antigen in 50 mM Α (pH: 8.0), 2 mM EDTA, for example the supernatant after treatment obtained in Example III.2 centrifugation and filtration through Benzonase, 0.45 μm membrane, is applied to a column equilibrated with 50 mM Tris-HCl (pH: 8.0), 2 mM EDTA, at a flow rate of approximately 10 ml/hour. Then, the column is washed with 20 volumes of 50 mM Tris-HCl (pH: 8.0), batch adsorption can be 2 mM EDTA. Alternatively, carried out, in which the mixture is left overnight at 5 ± 3 °C, with stirring.

The gel is washed with 2 to 6 volumes of 10 mM PBS buffer (pH: 6.8). The antigen is eluted with a 100 mM glycine buffer (pH: 2.5). The eluate is collected in 3 ml fractions, to which 150 μ l of 1 mM PBS buffer (pH: 8.0) are added. The optical density is

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measured at 280 nm for each fraction; those containing the antigen are recovered and stored at $-20\,^{\circ}\text{C}$.

Fragments of the genome of N. meningitidis Z2491 described in patent application WO 98/02547

	(2) INFORMATION FOR SEQ ID NO: 70A:	
5	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 243 base pairs	
	(B) TYPE: nucleotide	
	(C) STRANDEDNESS: single	
10	(D) TOPOLOGY: linear	
	(ii) MOLECULE TYPE: DNA (genomic)	
15	(iii) HYPOTHETICAL: NO	
15	(iv) ANTISENS: NO	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 70A:	
	GATCAGACCO ATTTTCAGCG CACCGTAAGC GCGGATTTTC TCGAATTTTT CCAAAGCTGC	60
	GGCATCGTTG TTGATGTCGT CTTGCAACTC TTTGCCCGTG TAGCCCAAGT CGGCGGCATT	120
	CAGGAAAACG GTCGGAATG: CCGCGTTGAT GAGCGTGGCT TTCAAACGGC CTATATTCGG	180
	CACATCAATT TCATCGACCA AATTGCCGGT TGGGAACATA CTGCCTTCGC CGTCGGCTGG	240
20	ATC	243
	(2) INFORMATION FOR SEQ ID NO: 73A:	
	(i) SEQUENCE CHARACTERISTICS:	
25	(A) LENGTH: 120 base pairs	
	(B) TYPE: nucleotide	
	(C) STRANDEDNESS: single	
	(D) TOPOLOGY: linear	
30	(ii) MOLECULE TYPE: DNA (genomic)	

(iii) HYPOTHETICAL: NO

	(IV) ANTISENS: NO	
5	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 73A:	
)	CGGTCAGAAA CAGGCAAGGT AATGAAAATG CCTGAGGCAC GGACTGTGCT GCGAACGAAA	60
	ACTCCTTACC GAAGTCTTCT ATACCCAGGC TCAATAGCCG CTCAAGGAGA GAGCTATCAT	120
	(2) INFORMATION FOR SEQ ID NO: 74A:	
10	(i) SEQUENCE CHARACTERISTICS:(A) LENGTH: 120 base pairs(B) TYPE: nucleotide(C) STRANDEDNESS: single(D) TOPOLOGY: linear	
15	(ii) MOLECULE TYPE: DNA (genomic)	
	(iii) HYPOTHETICAL: NO	
20	(iv) ANTISENS: NO	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 74A:	
	CGGTCAGAAA CAGGCAAGGT AATGAAAATG CCTGAGGCAC GGACTGTGCT GCGAACGAAA	60
	ACTOCTTACO GAAGTOTTOT ATACOCAGGO TOAATAGCOG CTCAAGGAGA GAGCTATCAT	120
25	(2) INFORMATION FOR SEQ ID NO: 77A	
30	(i) SEQUENCE CHARACTERISTICS:(A) LENGTH: 269 base pairs(B) TYPE: nucleotide(C) STRANDEDNESS: single(D) TOPOLOGY: linear	
	(ii) MOLECULE TYPE: DNA (genomic)	

(iii) HYPOTHETICAL: NO

	(iv) ANTISENS: NO	
5	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 77A:	
	CGGAGCATAA AATCGTTATT AAAGATAATG GTATAGGAAC GAGCTTCGAT GAAATCAATG	60
	ATTTTATTT GAGAATCGGT CGGAACAGAA GGGAAGAAAA ACAAGCCTCC CCGTGCGGAA	120
	GAATTCCAAC GGGTAAAAAA GGCCTTGGTA AATTGGCATT ATTCGGGCTT GGCAACAAAA	180
	TTGAAATTTC TACTATCCAG GGAAACGAAA GGGTTACTTT TACTTTGGAT TATGCAGAGA	240
	TTCGAAGAAG CAAGGGTATT TATCAACCG	269
10	(2) INFORMATION FOR SEQ ID NO: 80A:	
	(i) SEQUENCE CHARACTERISTICS:(A) LENGTH: 207 base pairs(B) TYPE: nucleotide(C) STRANDEDNESS: single	
15	(D) TOPOLOGY: linear	
	(ii) MOLECULE TYPE: DNA (genomic)	
20	(iii) HYPOTHETICAL: NO	
	(iv) ANTISENS: NO	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 80A:	
	CGGGTCGCTT TATTTTGTGC AGGCATTATT TTTCATTTTT GGCTTGACAG TTTGGAAATA	60
	TTGTGTATCG GGGGGGGTA TTTGCTGACG TAAAAAACTA TAAACGCCGC GCAAAATATG	120
	GCTGACTATA TTATTGACTT TGATTTTGTC CTGCGCGGTG ATGGATAAAA TCGCCAGCGA	180
25	TAAAGAATTT GCGAGAACCT GATGCCG	207

(2) INFORMATION FOR SEQ ID NO: 81A:

	(i)	SEQUENCE CHARACTERISTICS:	
		(A) LENGTH: 224 base pairs	
		(B) TYPE: nucleotide	
5		(C) STRANDEDNESS: single	
		(D) TOPOLOGY: linear	
	(ii)	MOLECULE TYPE: DNA (genomic)	
10	(iii)	HYPOTHETICAL: NO	
	(iv)	ANTISENS: NO	
15	(xi)	SEQUENCE DESCRIPTION: SEQ ID NO: 81A:	
	CGGCAACGAT TI	PGAGCTATC GCGGTTACGA CATTCTGGAT TTGGCACAAA AATGCGAGTT	60
	TGAAGAAGTC 30	CCACCTGC TGATTCACGG CCATCTGCCC AACAAATTCG AGCTGGCCGC	120
	TTATAAAACC AA	AGCTCAAAT CCATGCGCGG CCTGCCTATC CGTGTGATTA AAGTTTTGGA	180
	AAGCCTGCCT GC	DACATACCC ATCOGATGGA CGTAATGCGT ACCG	224
	(2) INFORM	ATION FOR SEQ ID NO: 87A:	
20	(i)	SEQUENCE CHARACTERISTICS:	
		(A) LENGTH: 273 base pairs	
		(B) TYPE: nucleotide	
		(C) STRANDEDNESS: single	
		(D) TOPOLOGY: linear	
25			
	(ii)	MOLECULE TYPE: DNA (genomic)	
	(iii)	HYPOTHETICAL: NO	
30	(iv)	ANTISENS: NO	
	(vi)	SECUENCE DESCRIPTION: SEC ID NO: 874:	

AATTTCCACC TATGCCCTAC GCAGCGATTA TCCGTGGTTT ACCCAAAGGG TGATTATGGC	60
AAAAGCGCGG GGTTGAGCGA CCGCCTTTTG TTGCCGGCGT TCAAACGGGT TTTGATAGGA	120
AATGCAGGCA CGAAGCCTCG GCTGATTGTG ATGCACCTGA TGGGTTCGCA CAGTGATTTT	180
TGCACACGTT TGGATAAGGA TGCGCGGCGG TTTCAGTATC AAACTGAAAA AATATCCTGC	240
TATGTTTCCA TCAATCGCGC AAACCGATAA ATT	273
(2) INFORMATION FOR SEQ ID NO: 88A:	
(i) SEQUENCE CHARACTERISTICS:(A) LENGTH: 270 base pairs(B) TYPE: nucleotide(C) STRANDEDNESS: single(D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: DNA (genomic)	
(iii) HYPOTHETICAL: NO	
(iv) ANTISENS: NO	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 88A:	
AATTOTTOOG CACGGGGAGG CTTGTTTTTC TTCCCTTCTG TTCCGACCGA TTCTCAAATA	60
AAAATCATTG ATTTCATCGA AGTTCATTCC TATACCATTA TCTTTAATAA CGATTTTATG	120
CTCCGGTTTA TCGAATAACC TAACTTCCAC TTCCGTAGCA CATGCATCGT AGGCATTCGC	180
TATCAACTCG GCAATCGCAG GAACAGTGTG CGAATACAAT CTTTACACCC AAATGTTCGA	240
TTACGGTTGG CTCGAAACTC AATTTCAATT	270
(2) INFORMATION FOR SEQ ID NO: 89A:	
(i) SEQUENCE CHARACTERISTICS:(A) LENGTH: 267 base pairs(B) TYPE: nucleotide(C) STRANDEDNESS: single	

(D) TOPOLOGY: linear

	(ii)	MOLECULE TYPE: DNA (genomic)	
5	(iii)	HYPOTHETICAL: NO	
	(iv)	ANTISENS: NO	
10	(xi)	SEQUENCE DESCRIPTION: SEQ ID NO: 89A:	
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	CGGCTCAATC A	ATAATGTAA CCGTTTCCGA CCAGAAACTT CAGGAACGTG CCGCGTTTGC	12
	CTTGGGCGTC A	CCAATGCCG TAAAAATCAG CAACCGCAGC AATGAAGGCA TACGCATCAA	18
	CTTTACCGCA A	CTGTGGGTA AGCGCGTGAC CAATGCTATG TTACCAGTGT AATCAGCACA	24
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15	(i)	SEQUENCE CHARACTERISTICS: (A) LENGTH: 308 base pairs (B) TYPE: nucleotide (C) STRANDEDNESS: single (D) TOPOLOGY: linear	
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	(ii)	MOLECULE TYPE: DNA (genomic)	
	(iii)	HYPOTHETICAL: NO	
25	(iv)	ANTISENS: NO	
	(xi)	SEQUENCE DESCRIPTION: SEQ ID NO: 94A:	

.....

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TGTGCCAAAT C	CAGAATGTC	GTAACCGCGA	TACGTC	TAAA	CGTTGCCGGT	ACGCAACGGT	120
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GTCGGGGTTT G	SAGTAGTTTC	AGTCATGGTA	TTTCTC	CTTT	GTGTTTTTAT	GGGTTTCGG	3 240
TTTTCAGACG A	CCGATGCGG	ATTTGTTGAA	AGGCAG'	TCTG	AAAGCGGTAA	ATCATTTTTC	300
AAACAATT .							308
2) INFORM	ATION F	OR SEQ I	D NO:	95	5A:		
(i)	SEQUEN	ICE CHARA	ACTERI	[ST]	CS:		
	(A) LE	NGTH: 28	6 bas	e p	airs		
	(D) max	DE		1 _			

5

(B) TYPE: nucleotide

- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

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- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO

15 (iv) ANTISENS: NO

> (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 95A:

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(2) INFORMATION FOR SEQ ID NO: 98A:

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(A) LENGTH: 316 base pairs

(B) TYPE: nucleotide

(C) STRANDEDNESS: single

	(D) TOPOLOGY: linear		
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	(iii) HYPOTHETICAL: NO		
1.0	(iv) ANTISENS: NO		
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	AAACGCCGCA GCAAAATATG GCTGACTATA TTATTGACTT TGATTTTGTC	CTGCGCGGTG	180
	ATGGATAAAA TCGCCAGCGA TAAAGATTTG CGAGAACCTG ATGCCGGCCT	GTTGTTGAAT	240
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	CCCACATTTT GGAAGC		316

10

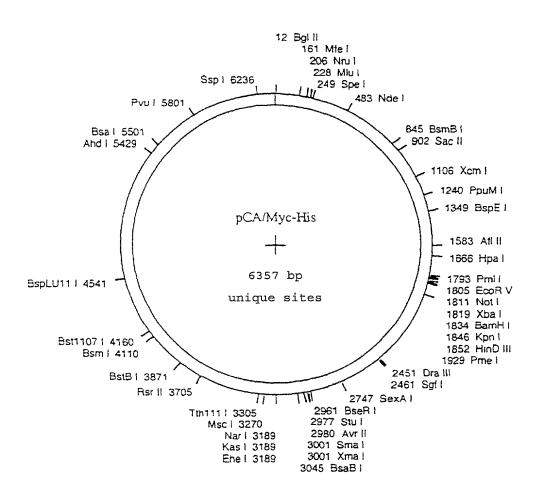
CLAIMS

- in isolated form, Nucleic acid 1. polypeptide specific for the pathogenic strains of the genus, antigenic fragment Neisseria orexcluding the sequences SEQ ID Nos 70A, 73A, 74A, 77A, 80A, 81A, 87A, 88A, 89A, 94A, 95A and 98A, the amino said specific polypeptide being acid sequence of identical or homologous to a sequence selected from the sequences of group II, group II consisting of sequences SEQ ID No. 2 to SEQ ID No. 52 (even numbers) and the sequence SEQ ID No. 53.
- Nucleic acid according to Claim 1, the nucleotide sequence of which is identical or homologous to a sequence selected from the sequences of group I, group I consisting of the sequences SEQ ID No. 1 to SEQ ID No. 51 (odd numbers).
- 3. Nucleic acid according to Claim 1, encoding a polypeptide specific for the pathogenic strains of the Neisseria genus, or antigenic fragment thereof, the amino acid sequence of said specific polypeptide being selected from the sequences SEQ ID Nos 55 to 77 (odd numbers).
- 4. Nucleic acid according to Claim 3, having a nucleotide sequence selected from the sequences SEQ ID Nos 54 to 76 (even numbers).
- 5. Polypeptide specific for the pathogenic strains of the *Neisseria* genus, and antigenic fragments thereof, the amino acid sequence of said specific polypeptide being identical or homologous to a sequence selected from the sequences of group II, consisting of the sequences SEQ ID No. 2 to SEQ ID No. 52 (even numbers) and the sequence SEQ ID No. 53.

15

- 6. Polypeptide according to Claim 5, specific for the pathogenic strains of the *Neisseria* genus, and antigenic fragments thereof, the amino acid sequence of said specific polypeptide being selected from the sequences SEQ ID Nos 55 to 77 (even numbers).
- 7. Expression vector comprising an expression cassette in which a nucleotide sequence as defined in one of Claims 1 to 4 is placed under conditions allowing its expression in a host cell.
- 10 8. Host cell transformed with the expression vector according to Claim 7.
 - 9. Pharmaceutical composition comprising:
 - a) a nucleic acid according to one of Claims 1 to 4, in naked form or in combination with at least one agent facilitating transfection;
 - b) or a vaccination vector comprising a nucleotide sequence as defined in one of Claims 1 to 4, such as in particular a virus or a bacterium;
- c) or a polypeptide according to either of 20 Claims 5 and 6;
 - optionally in combination with a pharmaceutically acceptable vehicle.
 - 10. Monospecific antibody directed against a polypeptide according to either of Claims 5 and 6.
- 25 11. Use of a nucleic acid according to one of Claims 1 to 4, or of a polypeptide specific for pathogenic Neisseria strains or of antigenic fragments thereof, according to either of Claims 5 and 6, for manufacturing a pharmaceutical composition intended for vaccination against Neisseria.

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	DECI	ARATION FOR USA PAT		
1	As a below named inventor, I hereby declare	(including Design and National that:	,	
	My residence, mailing address and citizenship a below) or an original, first and joint inventor (if	re as stated below adjacent to my name. It below a stated below of the subject	elieve I am the original, first and sole inventor (if or matter which is claimed and for which a patent is sou	
	on the invention entitled: Nucleic aci	ds and polypeptides spec	ific of the Neisseria genus ns	
	the specification of which:	pathogenic stra	ns	
	is attached hereto.		00/926	v 22
	<u>X</u> was filed on <u>26.04.2001</u>	as U.S. Application No	or PCT International Application No. 09/830	J433
		d on		
			fication, including the claims, as amended by any anability as defined in 37 CFR 1.56.	
	I hereby claim foreign priority benefits under 3 International application which designated at lea not claimed, any foreign application for patent o priority is claimedADDITIONAL APPLIC	5 U.S.C. 119(a)-(d) or 365(b) of any foreig ust one country other than the United States r inventor's certificate, or any PCT Internatic CATIONS IDENTIFIED ON ATTACHED:	n application(s) for patent or inventor's certificate, of America, listed below and have also identified be nal application, having a filing date before that of the SHEET)	or 365(a) of any PC low, where priority is application on which
	Prior Foreign Application No.	Country	Day/Month/Year Filed I	riority <u>Not</u> Claime
	FR 98 13693	FRANCE	30.10.98	
	I hereby claim the benefit under 35 U.S.C. 120 of matter of each claims of this application is not acknowledge the duty to disclose information we application and the national or PCT filing date of	f any U.S. application(s), or 365(c) of any Pt disclosed in the prior U.S. or PCT applic hich is material to patentability as defined in this applicationADDITIONAL APPL	CT application designating the U.S., listed below; and ation in the manner provided by the first paragraph 137 CFR 1.56 which became available between the IJCATIONS IDENTIFIED ON ATTACHED SHEET	insofar as the subject of 35 U.S.C. 112, filing date of the prio
	U.S. or PCT Parent Application No.	Parent Filing Date (Day/Month/Year)		
Ü	PCTFR99/02643	28.10,1999		
dura dina di ha dina dina dina dina dina dina dina din	As a named inventor, I hereby appoint the associated with Customer Number 000881 to Patent and Trademark Office connected therewit	registered practitioners of LARSON & prosecute this application and to transact a b Direct all correspondence to that Custom	TAYLOR, PLC Il business in the er Number.	t 60 <u>881</u>
La the ten ten ten ten ten ten ten	Direct all telephone calls to at TEL (703) 739-4 I hereby declare that all statements made herein further that these statements were made with the U.S.C. 1000 and that such willful false statemen	of my own knowledge are true and that a knowledge that willful false statements and	Il statements made on information and belief are be the like so made are punishable by fine or imprisonm on or any patent issued thereon.	lieved to be true; an
ū		SOLE OR	Citizenship	
- A	Given Name (first	TINVENTOR	French Family Name	
- G C	and Middle [if any]) Luc		or Surname AUJAME	
	Address 4// Chemin dii Pi	uits - 69210 FLEURIEUX :	SUR L'ABRESLE - FRANCE FRA	<u>×</u>
in the	(if different from PO address) same as	s above		
	DATE HERE Inventor's Signature	s above	Date 9.7. 2001	
	SECOND	JOINT INVENTOR (if any)	Citizenship French	
	Given Name (first	(ii any)	Family Name BOUCHARDON	
. o c	Full Mailing Address 7, rue Nicolai - Residence - City, State/Country		=RX	
	+ SIGN AND	s above	Date 31.7.2001	
	DATE HERE Inventor's Signature	7	Date 31. 7. 2001	
	THIRD J	OINT INVENTOR (if any)	Citizenship	
	Given Name (first and Middle [if any]) Geneviève	(i. u.i.j)	French Family Name or Surname <u>RENAULD-MON</u>	ICENTE
	Full Mailing	nboisiers - 69630 <u>CHAPO</u>		
	Residence - City, State/Country		UDI - FRANCE I I	
	SIGN AND	as above	42 07 90-	<u> </u>
	DATE HERE Inventor's Signature	G. Kenantolo	Date 10.07.2001	L
	FOURTH	JOINT INVENTOR (if any)	Citizenship	
	Given Name (first and Middle [if any]) Bachra	(·- ····)1	French Family Name or Surname ROKBT	
. 👓		- 69003 <u>LYON</u> - FRANCE		
	Residence - City, State/Country		FRX.	
	SIGN AND	as above	Date 11 0 7 20	
	DATE HERE Inventor's Signature			Z.,
	LABOON 6.	TAYLOR, PLC • 1199 North Fairfax Street	- Cuito 000 - Alexandria Virginia 20214	11/9

DECLARATION FOR USA PATENT APPLICATION

-jj-

(including Design and National Stage PCT)

ADDITIONAL INFORMATION SHEET (use as required)

	U.S. Provisional Application No.	Parent Filing Date (I	Day/Month/Year)	
	ior Foreign Application(s) Foreign Application No.	Country	Day/Month/Year Filed	Priority <u>Not</u> (
				- <u></u>
	U S.C. § 120 application(s). U.S. or PCT Parent Application No.	Parent Filing Date	(Day/Month/Year) Parent Pat	tent No. (if applicable)
-				
Additional Jo	int Inventor(s):			
Given Nam	FIFTH JOINT IN (if any)		Citizenship French Family Name MASSIE	2
and Middle Full Mailing	lifanyl) Xavier	rent 75015 PARTS	or Surname WASSII	-
Address	Cin State Country		- FRANCE FTEX	
Residence -	from DO address) Camp ac ah	OVE		
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I SIGN AND	RE Inventor's Signature SIXTH JOINT IN	WENTOR	Citizenship	,200
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Given Nam and Middle Full Mailing	RE Inventor's Signature SIXTH JOINT IN (if any) e (first [If any]) Colin	WENTOR	Citizenship British Family Name or Surname TINSLEY	
Given Nam and Middle Full Mailing Address	RE Inventor's Signature SIXTH JOINT IN (if any) e (first [if any]) Colin E 16, Square Jean Théba	wentor aud - 75015 <u>PARIS</u> -	Citizenship British Family Name or Surname TINSLEY	
Given Nam and Middle Full Mailin Address Residence (if different SIGN ANL	RE Inventor's Signature SIXTH JOINT IN (if any) e (first [If any]) Colin E 16, Square Jean Théba City, State/Country from PO address) same as abo	wentor aud - 75015 <u>PARIS</u> -	Citizenship British Family Name or Surname TINSLEY	Y
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Given Nam and Middle Full Mailin Address Given Nam and Middle Full Mailin Address Given Nam and Middle Full Mailin Address Residence (if different full Mailin Address)	RE Inventor's Signature SIX PA JOINT IN (if any) e (first [if any]) Colin g 16, Square Jean Théba City, State/Country from PO address) same as about RE Inventor's Signature SEVENTH JOINT (if any) e (first [if any]) Agnès g 33 bis, rue du Docteu City, State/Country from PO address) same as about	eud – 75015 <u>PARIS</u> ove Tinsley INVENTOR ur Roux – 75015 <u>PA</u>	Citizenship British Family Name or Surname TINSLEY FRANCE Date Citizenship French Family Name or Surname PERRI RIS - FRANCE	COT
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Given Nam and Middle Full Mailing Address Residence (if different SIGN ANI DATE HE	RE Inventor's Signature SIXTH JOINT IN (if any) e (first [If any]) Colin E 16, Square Jean Théba City, State/Country from PO address) same as about RE Inventor's Signature SEVENTH JOINT (if any) e (first [If any]) Agnès E 33 bis, rue du Docteu City, State/Country from PO address) same as about RE Inventor's Signature EIGHTH JOINT (if any) te (first [if any])	wentor aud - 75015 <u>PARIS</u> - ove Tinsley INVENTOR ur Roux - 75015 <u>PA</u>	Citizenship British Family Name or Surname TINSLEY Date Date Citizenship French Family Name or Surname PERRI RIS - FRANCE Date 1 9 June Citizenship Family Name Citizenship Family Name	COT
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PCT/FR99/02643

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115

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Leu Phe Asp Lys Pro Glu His Lys Ile Val Ile Lys Asp Asn Gly Ile

Gly Met Ser Phe Asp Glu Ile Asn Asp Phe Tyr Leu Arg Ile Gly Arg 65 70 75 80

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Lys Tyr Asp Leu Val Thr Pro Gln Phe Glu Trp Glu Tyr Gln Asp Leu 210 220

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gat	gca	ctt	cac	tta	aca	gta	ggt	acc	aac	gac	att	caa	tcc	ttt	gcg	816

Asp Ala Leu His Leu Thr Val Gly Thr Asn Asp Ile Gln Ser Phe Ala cga cat ttg cgc gac caa aac ctg atc cgc caa aac aat ggg aaa att Arg His Leu Arg Asp Gln Asn Leu Ile Arg Gln Asn Asn Gly Lys Ile 275 gaa tat gca cog ttt act gaa cot aaa coa cag coa acg coc aag cag Glu Tyr Ala Pro Phe Thr Glu Pro Lys Pro Gln Pro Thr Pro Lys Gln 295 cct aaa aaa acc gca tgg gaa cct gat gaa att att tgg aaa aaa gtg Pro Lys Lys Thr Ala Trp Glu Pro Asp Glu Ile Ile Trp Lys Lys Val 310 att gec geg tta teg tta aag aac egt eet aat aaa ace aaa act tta 1008 Ile Ala Ala Leu Ser Leu Lys Asn Arg Pro Asn Lys Thr Lys Thr Leu 330 cgc aat aca atc cag gca ctc aca aaa tcc aat gca caa gaa act gac Arg Asn Thr Ile Gln Ala Leu Thr Lys Ser Asn Ala Gln Glu Thr Asp 345 aaa ctg cta caa cat tta caa gat gac cca agt cct acg tat tga 1101 Lys Leu Leu Gln His Leu Gln Asp Asp Pro Ser Pro Thr Tyr

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<211> 366

<212> PRT

<213> Neisseria meningitidis

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Leu His Lys Met Leu Pro Ile Ser Leu Val Gln Ser Leu Leu Arg Phe 35 40 45

Gly Glu Arg Val His Leu Val Gln Leu Gln Lys Thr Gly Lys Asn Ala 50 60

Leu Asp Phe Tyr Leu Ser Tyr Tyr Leu Gly Gln Ile Thr Ala Thr Asp 65 70 80

Pro Asn Ala Gln Ile Gly Ile Leu Ser Arg Asp Gly Gly Tyr Asp Val

Leu Val Glu His Ile Leu Lys Asn His Gln Ala Lys Gly Ile Val Arg 100 105 110

Leu Ala Asn Ile Asp Glu Val Gln His Gln Lys Ile Ala Thr Glu Pro

Pro Ser Ala Leu Leu Glu Asn Thr Pro Gln Pro Glu Thr Thr Leu Lys 130 140 Pro Gln Gln Pro Leu Thr Ser Tyr Phe Gln Ala Ala Leu Thr Ala Leu 145 150 155 160

Arg Arg Pro Asp Ala Phe Arg Pro Cys Arg Leu His Asn Leu Arg Gln 165 170 175

Asn Leu Arg Lys His Ile Leu Ser Asp Leu Phe Lys Glu Lys Thr Asp 180 185 190

Glu Glu Cys Glu Ile Thr Thr Ala Asn Val Ile Asn Lys Leu Lys Ala 195 200 205

Gln Asn Phe Ile Ser Ile Asp Glu Gln Glu Thr Val Ser Tyr His Leu 210 215 220

Ser Asp Asn Asp.Leu Leu Gln Arg Ile Gln Arg His Ile Leu Ser Gln 225 230 235

Arg Pro Lys Thr Tyr Ala Asp Phe Gln Ala Val Val Gln Asn Arg Ala 245 250 255

Asp Ala Leu His Leu Thr Val Gly Thr Asn Asp Ile Gln Ser Phe Ala 260 265 270

Arg His Leu Arg Asp Gln Asn Leu Ile Arg Gln Asn Asn Gly Lys Ile 275 280 285

Glu Tyr Ala Pro Phe Thr Glu Pro Lys Pro Gln Pro Thr Pro Lys Gln 290 295 300

Pro Lys Lys Thr Ala Trp Glu Pro Asp Glu Ile Ile Trp Lys Lys Val 305 310 315

Ile Ala Ala Leu Ser Leu Lys Asn Arg Fro Asn Lys Thr Lys Thr Leu 325 330 335

Arg Asn Thr Ile Gln Ala Leu Thr Lys Ser Asn Ala Gln Glu Thr Asp 340 345 350

Lys Leu Gln His Leu Gln Asp Asp Pro Ser Pro Thr Tyr 355 360 365

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<212> DNA

<213> Neisseria meningitidis

<220>

<221>

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gcc .	agc	gaa	atc	gcc	tat,	cgc	ttt	gta	ttc	gga	att	gaa	acc	tta	ccg	96
Ala	Ser	Glu	Ile 20		Tyr	Arg	Phe	Val 25	P'ne	Gly	Ile	Glu	Thr 30	Leu	Pro	
gct Ala	gca Ala	aaa Lys 35	atg Met	gca Ala	gaa Glu	acg Thr	ttt Phe 40	gcg Ala	ctg Leu	aca Thr	ttt Phe	atg Met 45	att Ile	gct Ala	gcg Ala	144
ctg Leu	tat Tyr 50	Lei	ttt Phe	gcg Ala	egt Arg	tat Tyr 55	aag Lys	gct Ala	tcg Ser	cgg Arg	ctg Leu 60	ctg Leu	att Ile	gcg Ala	gtg Val	192
ttt Phe 65	tto Phe	: gcg	g tto A Phe	agc Ser	att Ile 70	att Ile	gcc Ala	aac Asn	aat Asn	gta Val 75	cat His	tat Tyr	gcg Ala	gtr Val	tat Tyr 80	240
caa Glr	agt Ser	tg: Tr	g ato Met	acg Thr	ggc	atc Ile	aat Asn	tat Tyr	tgg Trp 90	ctg Leu	arg Met	ctg Leu	aaa Lys	gag Glu 95	att Ile	288
acc Thr	gaa Glu	a gte 1 Va	c ggd	/ Ser	gcg Ala	ggc Gly	gcg Ala	tcg Ser 105	atg Met	ttg Leu	gat Asp	aag Lys	ttg Leu 110	tgg Trp	ctg Leu	336
cct Pro	gc	g tt a Le	g tgg u Trj 5	o Gly	gtg Val	ttg Leu	gaa Glu 120	gcc Val	atg Met	ttg Leu	ttt Phe	tgc Cys 125	agc Ser	ctt Leu	gcc Ala	384
aag Lys	tto Pho	e Ki	c cgt s Arg	i aag J Lys	acg Thr	cat His 135	tit Phe	tct Ser	gcc Ala	gat Asp	ata Ile 140	ctg Leu	ttt Phe	gcc Ala	tic Phe	432
cta Leu 145	Me:	g ct t Le	g atg u Me	g att	ttc Phe 150	Val	cgt Arg	tog Ser	ttc Phe	gac Asp 155	acg Thr	aaa Lys	caa Gln	gag Glu	cac His 160	480
ggt Gl}	at / Il	t to e Se	g cc	c aaa c Lys 165	Pro	aca Thr	tac Tyr	agc Ser	cgc Arg 170	Ile	aaa Lys	gcc Ala	aat Asn	tat Tyr 175	ttc Phe	528
ago Sei	tt Fh	c gg e Gl	t ta y Ty 18	r Phe	gto Val	gga Gly	cgc	gtg Val 185	ren F	ecg	tat Tyr	cag Gln	ttg Leu 190	ttt Phe	gat Asp	576
tta Le:	a ag 1 Se	c ag r Ar 19	g at g Il 5	t cco	gco Ala	ttt Phe	aag Lys 200	Gln	cct Pro	gct Ala	cca Pro	agc Ser 205	Lys	atc Ile	Gly 999	624
caq Gl:	g gg n Gl 21	y Se	ıt gt r Va	t can 1 Gl	a aat n Asr	ato lile 215	. Val	: ctg . Leu	att Ile	atg : Met	220 220	Glu	ago Ser	gaa Glu	agc Ser	672
gc: Al: 22:	a Al	g ca a Hi	it tt .s Le	g aa u Ly	g ctç s Lei 230	ı Phe	ggc Gly	tac Tyr	: gga	cgo Arg 235	g Glu	act Thr	tcg Ser	ccg Pro	Phe 240	720
tt. Le	a ac u Th	c co	g ct	g to u Se 24	r Gli	a gco n Ala	gat As <u>r</u>	tit Phe	aac Lys 250	Pro	g att	gtg Val	aaa Lys	caa Gln 255	Ser	768
ta	tįto	c g	sa go	c tt	t at	g act	gea	a gtç	tco	ctq	g ccc	agt	tt:	ttc	aat	816

Tyr	Ser		Gly 260	Phe	Met	Thr	Ala	Val 265	Ser	Leu	Pro	Ser	Phe 270	Phe	Asn	
gcg Ala	ata Ile	ccg Pro 275	cac Ĥis	gcc Ala	aac Asn	ggc	ttg Leu 280	gaa Glu	caa Gln	atc Ile	agc Ser	ggc Gly 285	Gly	gat Asp	act Thr	864
aat Asn	atg Met 290	ttc Phe	cgc Arg	ctc Leu	gcc Ala	aaa Lys 295	gag Glu	cag Gln	ggc Gly	tat Tyr	gaa Glu 300	acg Thr	tat Tyr	ttt Phe	tac Tyr	912
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aaa Lys	tgg Trp	ata Ile	gac Asp	cat His 325	ctg Leu	att Ile	cag Gln	ccg Pro	acg Thr 330	cag Gln	ctt Leu	ejà aac	tac Tyr	ggc Gly 335	aac Asn	1008
Gjà āãc	gac Asp	aat Asn	atg Met 340	ccc Pro	gat Asp	gag Glu	aag Lys	ctg Leu 345	ctg Leu	ccg Pro	ctg Leu	ttc Phe	gac Asp 350	aaa Lys	atc Ile	1056
aat Asn	ttg Leu	cag Gln 355	cag Gln	Gly ggc	agg Arg	cat Eis	ttt Phe 360	atc Ile	gtg Val	ttg Leu	cac His	caa Gln 365	cgt Arg	ggt Gly	tcg ser	1104
cac His	gcc Ala 370	cca Pro	tac Tyr	agc Ser	gca Ala	ttg Leu 375	ttg Leu	cag Gln	cct Pro	caa Gln	gat Asp 380	aaa Lys	gta Val	ttc Phe	ggc	1152
gaa Glu 385	ctt Leu	att Ile	gtg Val	gat Asp	aag Lys 390	tac Tyr	gac Asp	aac Asn	acc	atc Ile 395	cac His	aaa Lys	acc Thr	gac Asp	caa Gln 400	1200
atg Met	att Ile	caa Gln	acc Thr	gta Val 405	ttc Phe	gag Glu	cag Gln	ctg Leu	caa Gln 410	aag Lys	cag Gln	cct Pro	gac Asp	ggc Gly 415	aac Asn	1248
tgg Trp	ctg Leu	ttt Phe	gcc Ala 420	tat Tyr	acc Thr	t <i>c</i> c Ser	gat Asp	cat His 425	ggc	cag Gln	tat Tyr	gtt Val	cgc Arg 430	caa Gln	gat Asp	1296
atc Ile	tac Tyr	aat Asn 435	Gln	ggc	acg Thr	gtg Val	cag Gln 440	Pro	gac Asp	agc Ser	tat Tyr	cto Leu 445	Val	pro	ctg Leu	1344
gtg Val	ttg Leu 450	Tyr	ago Ser	tcg Ser	aat Asn	aag Lys 455	Ala	gtg Val	caa Gln	cag Gln	gct Ala 460	Ala	aac Asn	cag Gln	gct Ala	1392
ttt Phe 465	Ala	ect Pro	tgo Cys	gag	att Ile 470	Ala	ttc Phe	cat His	cag Gln	Gln 475	Lev	tca Ser	acg Thr	ttc Phe	ctg Leu 480	1440
att Ile	cac His	acg Thr	ttg Leu	ggc Gly 485	Туг	gat Asp	atg Met	ccs Pro	gtt Val 490	. Ser	ggt Gly	tgt Cys	cgc	gaa Glu 495	ggc	1488
															att	1536
Ser	Val	Thr	Gly 500	Asn	Leu	Ile	Thr	Gly 505	Asp	Ala	GŢĀ	Ser	Leu 1 510	Asn 1	ile	
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- <212> PRT
- <213> Neisseria meningitidis

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Leu Tyr Leu Phe Ala Arg Tyr Lys Ala Ser Arg Leu Leu Ile Ala Val 50 60

Phe Phe Ala Phe Ser Ile Ile Ala Asn Asn Val His Tyr Ala Val Tyr 65 70 75 80

Gln Ser Trp Met Thr Gly Ile Asn Tyr Trp Leu Met Leu Lys Glu Ile 85 90 95

Thr Glu Val Gly Ser Ala Gly Ala Ser Met Leu Asp Lys Leu Trp Leu 100 105 110

Pro Ala Leu Trp Gly Val Leu Glu Val Met Leu Phe Cys Ser Leu Ala 115 120 125

Lys Phe His Arg Lys Thr His Phe Ser Ala Asp Ile Leu Phe Ala Phe 130 140

Leu Met Leu Met Ile Phe Val Arg Ser Phe Asp Thr Lys Gln Glu His 145 \$150\$

Gly Ile Ser Pro Lys Pro Thr Tyr Ser Arg Ile Lys Ala Asn Tyr Phe 165 170 175

Ser Phe Gly Tyr Phe Val Gly Arg Val Leu Pro Tyr Gln Leu Phe Asp 180 185 190

Leu Ser Arg Ile Pro Ala Phe Lys Gln Pro Ala Pro Ser Lys Ile Gly
195 200 205

Gln Gly Ser Val Gln Asn Ile Val Leu Ile Met Gly Glu Ser Glu Ser 210 . 215 220

Ala Ala His Leu Lys Leu Phe Gly Tyr Gly Arg Glu Thr Ser Pro Phe 225 230 235

Leu Thr Arg Leu Ser Gln Ala Asp Phe Lys Pro Ile Val Lys Gln Ser

Tyr Ser Ala Gly Phe Met Thr Ala Val Ser Leu Pro Ser Phe Phe Asn 260 265 270

Ala Ile Pro His Ala Asn Gly Leu Glu Gln Ile Ser Gly Gly Asp Thr 275 280 285

Asn Met Phe Arg Leu Ala Lys Glu Gln Gly Tyr Glu Thr Tyr Phe Tyr 290 295 300

Ser Ala Gln Ala Glu Asr Glu Met Ala Ile Leu Asn Leu Ile Gly Lys 305 310 315 320

Lys Trp Ile Asp His Leu Ile Gln Pro Thr Gln Leu Gly Tyr Gly Asn 325 330 335

Gly Asp Asn Met Pro Asp Glu Lys Leu Deu Pro Leu Phe Asp Lys Ile 340 345 350

Asn Leu Gln Gln Gly Arg His Phe Ile Val Leu His Gln Arg Gly Ser 355 360 365

His Ala Pro Tyr Ser Ala Leu Leu Gln Pro Gln Asp Lys Val Phe Gly 370 380

Glu Leu Ile Val Asp Lys Tyr Asp Asn Thr Ile His Lys Thr Asp Gln 385 390 400

Met Ile Gln Thr Val Phe Glu Gln Leu Gln Lys Gln Pro Asp Gly Asn 405 410 415

Trp Leu Phe Ala Tyr Thr Ser Asp His Gly Gln Tyr Val Arg Gln Asp 420 425 430

Ile Tyr Asn Gln Gly Thr Val Gln Pro Asp Ser Tyr Leu Val Pro Leu 435 440 445

Val Leu Tyr Ser Ser Asn Lys Ala Val Gln Gln Ala Ala Asn Gln Ala 450 455 460

Phe Ala Pro Cys Glu Ile Ala Phe His Gln Gln Leu Ser Thr Phe Leu 465 470 475 480

Ile His Thr Leu Gly Tyr Asp Met Pro Val Ser Gly Cys Arg Glu Gly 485 490 495

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Arg Asp Gly Lys Ala Glu Tyr Val Tyr Pro Gln 515

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<211> 3204

<212> DNA

<213> Neisseria meningitidis

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<222> (1)..(3201)

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atg g Met A	cg : la I	ta Leu	gct Ala 20	gtt Val	gca Ala	aca Thr	aca Thr	ctt Leu 25	tct Ser	gcc Ala	tgc Cys	tta Leu	ggc Gly 30	ggc Gly	Gly	96
ggc g Gly G	ijà , làc :	act Thr 35	tct Ser	gcg Ala	ecc Pro	gac Asp	ttc Phe 40	aat Asn	gca Ala	ggc	Gly	acc Thr 45	ggt Gly	atc Ile	ggc Gly	144
agc a Ser A	ac Asn 50	agc Ser	aga Arg	gca Ala	aca Thr	aca Thr 55	gcg Ala	aaa Lys	tca Ser	gca Ala	gca Ala 60	gta Val	tct Ser	tac Tyr	gcc Ala	192
ggt a Gly 1 65	atc [le	aag Lys	aac Asn	gaa Glu	atg Met 70	tgc Cys	aaa Lys	gac Asp	aga Arg	agc Ser 75	atg Met	ctc L e u	tgt Cys	gcc Ala	80 GJÀ āār	240
cgg (Arg)	gat Asp	gac Asp	gtt Val	gcg Ala 85	gtt Val	aca Thr	gac Asp	agg Arg	gat Asp 90	gcc Ala	aaa Lys	atc Ile	aat Asn	gcc Ala 95	CCC Pro	288
ccc (Pro	ccg Pro	aat Asn	ctg Leu 100	cat His	acc Thr	gga Gly	gac Asp	ttt Phe 105	aca Thr	aac Asn	cca Pro	aat Asn	gac Asp 110	HIA	tac Tyr	336
aag Lys	aat Asn	ttg Leu 115	atc Ile	aac Asn	ctc Leu	aaa Lys	Pro 120	Ala	att Ile	gaə Glu	gca Ala	ggc Gly 125	Түч	aca Thr	. Gly	384
Arg	130 GJÀ 888	gta Val	gag Glu	gta Val	ggt Gly	ato Ile 135	. Val	gat Asp	aca Thi	ggq Giy	gaa Glu 140	ı Ser	gto Val	ggo Gly	: agc / Ser	432
ata Ile 145	tcc Ser	ttt Phe	ccc Pro	gas Glu	ctg Leu 150	Tyr	: Gly	aga Arg	aaa g Lys	gaa Glu 15	1 H1	c ggo s Gly	tat Ty	aac Asi	gaa Glu 160	480
aat Asn	tac Tyr	aaa Lys	aac Asi	: tat 1 Tyr 165	Th:	gcg Ala	g tat a Ty:	ato Met	g cgg E Arg 17	3 PA:	g ga s Gl	a gcg	g cct	ga: 0 Gl : 17.	a gac ı Asp	528
gga Gly	Gly	ggt ggt	aaa Ly:	s Asp	att p Ile	aaa a Lys	a gc	t tct a Sei 185	r Ph	c ga e As	c ga p As	t gaq p Gli	g gc 1 Al 19	a va	t ata 1 Ile	576
gag Glu	act Thr	gaa Glu 199	ı Al	a aag a Lys	g ccq s Pro	g ac	g ga r As 20	p Il	c cg e Ar	c ca g Hi	c gt s Va	a aa 1 Ly 20	g GI	a at u Il	c gga e Gly	624
cac His	ato Ile 210	As	t gt p Va	g gt l Va	c tc	c ca r Hi 21	s Il	t at e Il	t gg e Gl	c gg y Gl	g cg y Ar 22	g Se	c gt r Va	g ga .1 As	b GJA	672

						gcg Ala										720
						aac Asn										768
						gaa Glu										816
						gca Ala										864
						cgc Arg 295										912
			-			atc Ile	_	_	-			-	_			960
	-					cgt Arg				_					_	1008
						gct Ala										1056
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cgt Arg	aca Thr	aac Asn	ccg Pro	att Ile 405	caa Gln	att Ile	gcc Ala	gga Gly	aca Thr 410	tcc Ser	ttt Phe	tcc Ser	gca Ala	ccc Pro 415	atc Ile	1248
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gca Ala	gtc Val 450	ggc Gly	gtg Val	gac Asp	agc Ser	aag Lys 455	t:c Phe	ggc	tgg Trp	gga Gly	ctg Leu 460	ctg L e u	gat Asp	gcg Ala	ggt Gly	1392

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acc Thr	gtg Val	cac His	ats Ile 580	Lys	ggc Gly	gat Asp	ctg Leu	cag Gln 585	ctg Leu	ggc Gly	Gly	gaa Glu	ggt Gly 590	acg Thr	ctg Leu	1776
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aac Asn 625	Arg	acc Thr	gga Gly	caa Glr	cgt Arg 630	Val	ccc Pro	ttc Phe	ctg Lev	agt Ser 635	: Ala	gcc Ala	aaa Lys	ato Ile	999 Gly 640	1920
Arç	gat J Asp	tat Tyr	tct Ser	2 11 c Phe 64 3	Phe	aca Thr	aac Asn	ato Ile	gaa Glu 650	Thr	gad Asp	ggt Gly	. Gl ⁾	teto Lev 655	g ctg 1 Leu 5	1968
gct Ala	tco a Ser	cto Lev	gad 1 Asp 660	Ser	gto Val	gaa Glu	aaa Lys	aca Thi	Ala	617 1 330	c agt / Sei	gaa Glu	gg Gly 670	/ Asy	acg o Thr	2016
. ctç Le:	g tco 1 Sei	tat Ty:	r Ty	gto Vai	c cgt l Arg	a Arg	680 Gl7	/ Asi	geç n Ala	g gca A Ala	a cgg	g act Thi 685	- Ala	t tog a Se:	g gca r Ala	2064
gcg	g gca a Ala 69	a Hi	t tc: s Se:	c gcgr Al	g cco	gco Ala 699	a Gly	ctq Le	g aas	a cas	c gc s Al 70	a Va.	a ga l Gl	a cag u Gl:	g ggc n Gly	2112

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gta Val	cag Gln	cat His 755	gcg Ala	aat Asn	gcc Ala	gcc Ala	gac Asp 760	ggt Gly	gta Val	cgc Arg	atc Ile	ttc Phe 765	aac Asn	agt Ser	ctc Leu	2304
gcc Ala	gct Ala 770	acc Thr	gtc Val	tat Tyr	gcc Ala	gac Asp 775	agt Ser	acc Thr	gcc Ala	gcc Ala	cat His 780	gcc Ala	gat Asp	atg Met	cag Gln	2352
gga Gly 785	cgc Arg	cgg Arg	ctg Leu	aaa Lys	gcc Ala 790	gta Val	tcg Ser	gac Asp	GJÀ āāā	ttg Leu 795	gac Asp	cac Hìs	aac Asn	gct Ala	acg Thr 800	2400
ggt Gly	ctg Leu	cgc Arg	gtc Val	atc Ile 805	gcg Ala	çaa Gln	acc Thr	caa Gln	cag Gln 810	gac Asp	ggt Gly	gga Gly	acg Thr	tgg Trp 815	gaa Glu	2448
cag Gln	gj ggc	ggt Gly	gtt Val 820	gaa Glu	ggc Gly	aaa Lys	aig Met	cgc Arg 825	ggc	agt Ser	acc Thr	caa Gln	acc Thr 830	gtc Val	ggc	2496
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atg Met	gga Gly 850	His	agc Ser	aca Thr	tgg Trp	agc Ser 855	Glu	aac Asn	agt Ser	gca Ala	aat Asn 860	gca Ala	aaa Lys	acc Thr	gac	2592
ago Ser 865	Ile	agt Ser	: ctg	ttt Phe	gca Ala 870	Gly	ata Ile	cgg Arg	cac His	gat Asp 875	Ala	. Gly	gat Asp	ato Ile	ggc Gly 880	2640
tat Tyr	: ctc	aaa Lys	ggo Gly	ctg Leu 885	Phe	tcc Ser	tac Tyr	gga Gly	cgc Arg 890	Туг	aaa Lys	aac Asn	ago Ser	ato Ile 895	agc Ser	2688
Arg	ago Ser	acc Thr	900 900	/ Ala	gac Asp	gaa Glu	cat His	gcg Ala 905	Gli	a ggo ı Gly	ago Ser	gto Val	aac Asr 910	ı Gly	acg Thr	2736
. ct <u>c</u> Lei	g ato 1 Met	Glr 915	ı Lev	ı Gl ⁾ A add	gca Ala	ctç Lei	g ggc 1 Gly 920	/ Gly	gto / Val	c aac L Asi	gtt 1 Val	2 ccc 1 Pro 925	Phe	gco Ala	gca Ala	2784
acç Thi	930 930 930	/ As	tto D Lev	g acq ı Thi	g gto Val	gaa Glu 935	ı Gly	ggt Gly	cto Lev	ı Arg	tac Ty:	r Ası	c cto	g cto 1 Lei	c aaa 1 Lys	2832

cag gat gca ttc gcc gaa aaa ggc agt gct ttg ggc tgg agc ggc aac Gln Asp Ala Phe Ala Glu Lys Gly Ser Ala Leu Gly Trp Ser Gly Asn 2928 ago oto act gaa ggo aca otg gto gga oto gog ggt otg aag otg tog Ser Leu Thr Glu Gly Thr Leu Val Gly Leu Ala Gly Leu Lys Leu Ser 970 caa coc ttg ago gat aaa goo gto otg ttt goa acg gog ggo gtg gaa Gln Pro Leu Ser Asp Lys Ala Val Leu Phe Ala Thr Ala Gly Val Glu 985 ege gae etg aac gga ege gae tae aeg gta aeg gge gge ttt aec gge 3024 Arg Asp Leu Asn Gly Arg Asp Tyr Thr Val Thr Gly Gly Phe Thr Gly 3072 geg act gea gea ace gge aag acg ggg gea ege aat atg eeg cac ace Ala Thr Ala Ala Thr Gly Lys Thr Gly Ala Arg Asn Met Pro His Thr 1015 3120 ege etg gtt gee ggt etg gge geg gat gte gaa tte gge aac gge tgg Arg Leu Val Ala Gly Leu Gly Ala Asp Val Glu Phe Gly Asn Gly Trp 1035 1030 aac ggc ttg gca cgt tac agc tac gcc ggt tcc aaa cag tac ggc aac 3168 Asn Gly Leu Ala Arg Tyr Ser Tyr Ala Gly Ser Lys Gln Tyr Gly Asn 1050 1045 cac ago gga oga gto ggo gta ggo tac ogg tto tga 3204 His Ser Gly Arg Val Gly Val Gly Tyr Arg Phe 1060 1065

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<211> 1607

<212> PRT

<213> Neisseria meningitidis

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 Cys Leu Gly Gly Gly Gly
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 25
 30

 Gly Gly Thr Ser Ala Pro Asp Phe Asn Ala Gly Gly Thr Gly Ile Gly 35
 40
 45
 45

 Ser Asn Ser Arg Ala Thr Thr Ala Lys Ser Ala Ala Val Ser Tyr Ala 50
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 Gly Ile Lys Asn Glu Met Cys Lys Asp Arg Ser Met Leu Cys Ala Gly 65
 70
 75
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 Arg Asp Asp Val Ala Val Thr Asp Arg Asp Ala Lys Ile Asn Ala Pro 90
 95

 Pro Pro Asn Leu His Thr Gly Asp Phe Thr Asn Pro Asn Asp Ala Tyr 100
 105
 110

Lys Asn Leu Ile Asn Leu Lys Pro Ala Ile Glu Ala Gly Tyr Thr Gly
115 120 125

Arg Gly Val Glu Val Gly Ile Val Asp Thr Gly Glu Ser Val Gly Ser 130 140

Ile Ser Phe Pro Glu Leu Tyr Gly Arg Lys Glu His Gly Tyr Asn Glu 145 150 155

Asn Tyr Lys Asn Tyr Thr Ala Tyr Met Arg Lys Glu Ala Pro Glu Asp 165 170 175

Gly Gly Lys Asp Ile Lys Ala Ser Phe Asp Asp Glu Ala Val Ile 180 185 190

Glu Thr Glu Ala Lys Pro Thr Asp Ile Arg His Val Lys Glu Ile Gly
195 200 205

His Ile Asp Val Val Ser His Ile Ile Gly Gly Arg Ser Val Asp Gly 210 215 220

Arg Pro Ala Gly Gly Ile Ala Pro Asp Ala Thr Leu His Ile Met Asn 225 230 235

Thr His Asp Gly Thr Lys Asn Glu Ile Met Ser Ala Ala Ile Arg Asn 245 250 255

Ala Trp Val Lys Leu Gly Glu Arg Gly Val Arg Ile Val Asn Asn Ser 260 265 270

Phe Gly Thr Thr Ser Arg Ala Gly Thr Ala Asp His Phe Gln Ile Ala 275 280 285

Asn Ser Glu Glu Gln Tyr Arg Gln Ala Leu Leu Ala Tyr Ser Gly Gly 290 295 300

Asp Lys Thr Asp Glu Gly Ile Arg Leu Met Gln Gln Ser Asp Tyr Gly 305 310 315

Asn Leu Ser Tyr His Ile Arg Asn Lys Asn Met Leu Phe Ile Phe Ser 325 330 335

Ala Ser Asn Asp Ala Gln Ala Gln Pro Asn Thr Leu Thr Leu Deu Pro 340 345 350

Phe Tyr Glu Lys Asp Ala Gln Lys Gly Ile Ile Thr Val Ala Gly Val 355 360 365

Asp Arg Ser Gly Glu Lys Phe Asn Gly Ser Asn His Cys Gly Ile Thr 370 375 380

Ala Met Trp Cys Leu Ser Ala Pro Tyr Glu Ala Ser Val Arg Phe Thr 385 390 395 400

Arg Thr Asn Pro Ile Gln Ile Ala Gly Thr Ser Phe Ser Ala Pro Ile 405 410 415

Val Thr Gly Thr Ala Ala Leu Leu Leu Gln Lys Tyr Pro Trp Met Ser 420 425 430 $\frac{1}{2^{n-1}} \left(\frac{1}{n} + \frac{1}{n} \right) = \frac{1}{2^{n-1}} \left(\frac{1}{n} + \frac{1}{n} \right) = \frac{1}{2^{n-1}} \left(\frac{1}{n} + \frac{1}{n} \right)$

Asn Asp Asn Leu Arg Thr Thr Leu Leu Thr Thr Ala Gln Asp Ile Gly
435
440

Ala Val Gly Val Asp Ser Lys Phe Gly Trp Gly Leu Leu Asp Ala Gly 450 455

Lys Ala Met Asn Gly Pro Ala Ser Phe Pro Phe Gly Asp Phe Thr Ala 465 470 475 480

Asp Thr Lys Gly Thr Ser Asp Ile Ala Tyr Ser Phe Arg Asn Asp Ile 485 490 495

Ser Gly Thr Gly Gly Leu Ile Lys Lys Gly Gly Ser Gln Leu Gln Leu 500 505 510

His Gly Asn Asn Thr Tyr Thr Gly Lys Thr Ile Ile Glu Gly Gly Ser 515 520 525

Leu Val Leu Tyr Gly Asn Asn Lys Ser Asp Met Arg Val Glu Thr Lys 530 540

Gly Ala Leu Ile Tyr Asn Gly Ala Ala Ser Gly Gly Ser Leu Asn Ser 545 550 555 560

Asp Gly Ile Val Tyr Leu Ala Asp Thr Asp Arg Ser Gly Ala Asn Glu 565 570 575

Thr Val His Ile Lys Gly Asp Leu Gln Leu Gly Gly Glu Gly Thr Leu 580 585 590

Tyr Thr Arg Leu Gly Lys Leu Leu Lys Val Asp Gly Thr Ala Met Thr 595 600 605

Gly Gly Lys Leu Tyr Met Ser Ala Arg Gly Lys Gly Ala Gly Tyr Leu 610 620

Asn Arg Thr Gly Gln Arg Val Pro Phe Leu Ser Ala Ala Lys Ile Gly 625 630 635 640

Arg Asp Tyr Ser Phe Phe Thr Asn Ile Glu Thr Asp Gly Gly Leu Leu 645 650 655

Ala Ser Leu Asp Ser Val Glu Lys Thr Ala Gly Ser Glu Gly Asp Thr 660 665 670

Leu Ser Tyr Tyr Val Arg Arg Gly Asn Ala Ala Arg Thr Ala Ser Ala 675 680 685

Ala Ala His Ser Ala Pro Ala Gly Leu Lys His Ala Val Glu Gln Gly 690 695 700

Gly Ser Asn Leu Glu Asn Leu Met Val Glu Leu Asp Ala Ser Glu Ser . 705 710 715 720

Ser Ala Thr Pro Glu Thr Val Glu Thr Ala Ala Ala Asp Arg Thr Asp $725 \hspace{1cm} 730 \hspace{1cm} 735$

Met Pro Gly Ile Arg Pro Tyr Gly Ála Thr Phe Arg Ala Ala Ala Ala 740 745 750

Val Gln His Ala Asn Ala Ala Asp Gly Val Arg Ile Phe Asn Ser Leu 755 760 765

Ala Ala Thr Val Tyr Ala Asp Ser Thr Ala Ala His Ala Asp Met Gln 770 780

Gly Arg Arg Leu Lys Ala Val Ser Asp Gly Leu Asp His Asn Ala Thr 785 790 795 800

Gly Leu Arg Val Ile Ala Gln Thr Gln Gln Asp Gly Gly Thr Trp Glu 805 810 815

Gln Gly Val Glu Gly Lys Met Arg Gly Ser Thr Gln Thr Val Gly 820 825 830

Ile Ala Ala Lys Thr Gly Glu Asn Thr Thr Ala Ala Ala Thr Leu Gly 835 840

Met Gly His Ser Thr Trp Ser Glu Asn Ser Ala Asn Ala Lys Thr Asp 850 855 860

Ser Ile Ser Leu Phe Ala Gly Ile Arg His Asp Ala Gly Asp Ile Gly 865 870 875 880

Tyr Leu Lys Gly Leu Phe Ser Tyr Gly Arg Tyr Lys Asn Ser Ile Ser 885 890 895

Arg Ser Thr Gly Ala Asp Glu His Ala Glu Gly Ser Val Asn Gly Thr 900 905 910

Leu Met Gln Leu Gly Ala Leu Gly Gly Val Asn Val Pro Phe Ala Ala 915 920 925

Thr Gly Asp Leu Thr Val Glu Gly Gly Leu Arg Tyr Asp Leu Leu Lys 930 935 940

Gln Asp Ala Phe Ala Glu Lys Gly Ser Ala Leu Gly Trp Ser Gly Asn 945 950 955 960

Ser Leu Thr Glu Gly Thr Leu Val Gly Leu Ala Gly Leu Lys Leu Ser 965 970 975

Gln Pro Leu Ser Asp Lys Ala Val Leu Phe Ala Thr Ala Gly Val Glu 980 985 990

Arg Asp Leu Asn Gly Arg Asp Tyr Thr Val Thr Gly Gly Phe Thr Gly 995 1000 2005

Ala Thr Ala Ala Thr Gly Lys Thr Gly Ala Arg Asn Met Pro His Thr 1010 1015 1020

Arg Leu Val Ala Gly Leu Gly Ala Asp Val Glu Phe Gly Asn Gly Trp
025 1030 1035 1040

Asn Gly Leu Ala Arg Tyr Ser Tyr Ala Gly Ser Lys Gln Tyr Gly Asn 1045 1050 1055

His Ser Gly Arg Val Gly Val Gly Tyr Arg Phe 1060 1065

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<211> 339

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112 <211>

<212> PRT

Neisseria meningitidis <213>

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. Ala Gly Cys Gly Ser Ile Asn Asn Val Thr Val Ser Asp Gln Lys Leu 20

Gln Glu Arg Ala Ala Phe Ala Leu Gly Val Ser Gln Asn Ala Val Lys 40

Ile Ser Asn Arg Ser Asn Glu Ser Ile Arg Ile Asn Phe Thr Ala Thr

Val Gly Lys Arg Val Ser Gln Cys Tyr Val Thr Ser Val Ile Ser Thr

75

65		70		75		80								
Ile Gly		hr Ser As 85	sp Ala I	le Cys Leu 90	Gly Gly G	ly Thr His 95								
Lys Gly	Lys Ser G 100	ln Cys As		eu Leu Lys 05		ly Arg Cys 10								
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ctg ctg : Leu L eu '	acg gaa aa: Thr Glu Ly: 20	a gtg tcg s Val Ser	ccc atc Pro Ile 25	atc gca tta Ile Ala Leu	atc ttg gtg Ile Leu Val	g ccg 96 L Pro								
ctg ttt (Leu Phe (ggg gcg tt Gly Ala Le 35	g ctg gcg u Leu Ala	ggg ttt Gly Phe 40	gat gta tcc Asp Val Ser	caa tta aaa Gln Leu Lys 45	a gaa 144 s Glu								
ttt tat Phe Tyr 50	tog ggc gg Ser Gly Gl	c acc aaa y Thr Lys 55	tog gtg Ser Val	atg cag att Met Gln Ile 60	gtg att atg Val Ile Me	g ttt 192 t Phe								
atg ttt Met Phe 65	toc att tt Ser Ile Le	g ttt ttt u Phe Phe 70	gga atc Gly Ile	atg aac gat Met Asn Asp 75	gtg ggg ct Val Gly Le	g ttc 240 u Phe 80								
cgt ccg Arg Pro	atg ata gg Met Ile Gl 8	y Gly Leu	att aag Ile Lys	ctg act cgg Leu Thr Arg 90	ggt aat at Gly Asn Il 9	e Val								
gca gtg Ala Val	agt gtg gg Ser Val Gl 100	g acg gtc y Thr Val	ttg gtg Leu Val 105	tog gtg gtg Ser Val Val	gcg cag tt Ala Gln Le 110	g gac 336 u Asp								
Gly Ala	ggt gcg ac Gly Ala Th	g acg ttt r Thr Phe	tta ttg Leu Leu 120	gtc gtc ccc Val Val Pro	gcc ctt tt Ala Leu Le 125	g ccg 384 u Pro								
ctt tac Leu Tyr 130	aag cgt ct Lys Arg Le	g cat atg u His Met 135	aat cct Asn Pro	tac ctg ctg Tyr Leu Leu 140	Phe Leu Le	g ctg 432 u Leu								

act tcc agt gcg gga ttg att aac ctt ctg ccg tgg ggc ggg ccg acc

	Thr 145	Ser	Ser	Ala	Gly	Leu 150	Ile	Asn	Leu	Leu	Pro 155	Trp	Gly	Gly	Pro	Thr 160	
	ejā aaa	cgg Arg	gtt Val	gca Ala	agc Ser 165	gtg Val	ttg Leu	gly	gca Ala	gat Asp 170	gtg Val	ggc Gly	gaa Glu	ttg Leu	tat Tyr 175	aaa Lys	528
	cct Pro	ttg Leu	ttg Leu	acg Thr 180	gtg Val	caa Gln	att Ile	atc Ile	ggt Gly 185	gtg Val	gtg Val	ttt Phe	atc Ile	ctt Leu 190	gcg Ala	ctg Leu	576
	tcc Ser	ctg Leu	ctt Leu 195	ttg Leu	ggt Gly	gtg Val	cgt Arg	gaa Glu 200	aaa Lys	agg Arg	cgg Arg	att Ile	gtc Val 205	cgg Arg	gag Glu	ttg Leu	624
	ggc	gcg Ala 210	ttg Leu	ccc Pro	gcc	gtg Val	gcg Ala 215	gat Asp	ttg Leu	ata Ile	aag Lys	ccg Pro 220	gtg Val	cct Pro	ttg Leu	ccg Ser	672
	gaa Glu 225	gaa Glu	gaa Glu	caa Gln	aaa Lys	ttg Leu 230	gcg Ala	cgt Arg	ccg Pro	aaa Lys	ctg Leu 235	ttt Phe	tgg Trp	tgg Trp	aat Asn	gtc Val 240	720
	ctg Leu	ctg Leu	ttt ⊋he	ttg Leu	gcg Ala 245	gcg Ala	atg Met	agc Ser	ctg Leu	ctt Leu 250	ttt Phe	tcg Ser	ggc	atc Ile	ttc Phe 255	ccg Pro	768
	Pro	ggt Gly	tat Tyr	gta Val 260	ttt Phe	atg Met	ctg Leu	gct Ala	gca Ala 265	acg Thr	gcg Ala	gcg Ala	ttg Leu	ctt Leu 270	ttg Leu	aat Asn	816
	tac Tyr	cgc Arg	agc Ser 275	ccg Prc	cag Gln	gaa Glu	cag Gln	atg Met 280	gag Glu	cgg Arg	att Ile	tat Tyr	gcc Ala 285	cac Kis	gcc	gjå aac	864
	Gly	gcg Ala 290	gtg Val	atg Met	atg Met	gcg Ala	tcc Ser 295	a:t Ile	att Ile	ttg Leu	gcg Ala	gca Ala 300	ggt	acg Thr	ttt Phe	ttg Leu	912
	305 Gly 999	att	ttg Leu	aag Lys	ggt Gly	gcg Ala 310	Gly 999	atg Met	ttg Leu	gac Asp	gcg Ala 315	att Ile	tcc Ser	aaa Lys	gac Asp	att Ile 320	960
	gtg Val	cat Kis	atc Ile	ctg Leu	ccg Pro 325	gac Asp	gcg Ala	ctg Leu	ctg Leu	cct Pro 330	tat Tyr	ctg Leu	cat His	att Ile	gcc Ala 335	atc Ile	1008
	ggt Gly	gtg Val	ttg Leu	ggc Gly 340	att Ile	ccg Pro	ctt Leu	gag Glu	ttg Leu 345	gtt Val	ttg Leu	agt Ser	acg Thr	gac Asp 350	gct Ala	tat Tyr	1056
•	tat Tyr	ttc Phe	gga Gly 355	ctg Leu	ttt Phe	ccg Pro	att Ile	gtg Val 360	gag Glu	cag Gln	att Ile	acc Thr	tcg Ser 365	cag Gln	gcg Ala	gly ggc	1104
	gtg Val	gcg Ala 370	ccc Pro	gaa Glu	gca Ala	gca Ala	ggt Gly 375	tat Tyr	gcg Ala	atg Met	ttg Leu	atc Ile 380	ggc Gly	agt Ser	atc Ile	gtc Val	1152
	ggc	act	ttt	gtt	acg	cag	ctt	tcg	ccg	gct	ttg	tgg	atg	ggc	ttg	ggt	1200

Gly Thr Phe Val Thr Pro Leu Ser Pro Ala Leu Trp Met Gly Leu Gly 385 390 395 400

ttg gcg aaa ttg tcg atg ggc aaa cac atc cgt tat tcg ttt ttt tgg 1248 Leu Ala Lys Leu Ser Met Gly Lys His Ile Arg Tyr Ser Phe Phe Trp 405 410 415

gcg tgg ggt ttg tcg ctg gcg ata ttg gcc agt tcg ata gcg gca gga 1296
Ala Trp Gly Leu Ser Leu Ala Ile Leu Ala Ser Ser Ile Ala Ala Gly
420 425

atc gtg cct ctg ccg taa Ile Val Pro Leu Pro 435 1314

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<211> 437

<212> PRT

<213> Neisseria meningitidis

<400> 12

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Leu Leu Thr Glu Lys Val Ser Pro Ile Ile Ala Leu Ile Leu Val Pro $20 \\ 25 \\ 30$

Leu Phe Gly Ala Leu Leu Ala Gly Phe Asp Val Ser Gln Leu Lys Glu 35 40

Phe Tyr Ser Gly Gly Thr Lys Ser Val Met Gln Ile Val Ile Met Phe 50 60

Met Phe Ser Ile Leu Phe Phe Gly Ile Met Asn Asp Val Gly Leu Phe 65 70 75 80

Arg Pro Met Ile Gly Gly Leu Ile Lys Leu Thr Arg Gly Asn Ile Val 85 90 95

Ala Val Ser Val Gly Thr Val Leu Val Ser Val Val Ala Gln Leu Asp 100 105 110

Gly Ala Gly Ala Thr Thr Phe Leu Leu Val Val Pro Ala Leu Leu Pro 115 120 125

Leu Tyr Lys Arg Leu His Met Asn Pro Tyr Leu Leu Phe Leu Leu 130 140

Thr Ser Ser Ala Gly Leu Ile Asn Leu Leu Pro Trp Gly Gly Pro Thr 145 150 155 160

Gly Arg Val Ala Ser Val Leu Gly Ala Asp Val Gly Glu Leu Tyr Lys 165 170 175

Pro Leu Leu Thr Val Gln Ile Ile Gly Val Val Phe Ile Leu Ala Leu 180 185 190

Ser Leu Leu Gly Val Arg Glu Lys Arg Arg Ile Val Arg Glu Leu
195 200 205

Gly Ala Leu Pro Ala Val Ala Asp Leu Ile Lys Pro Val Pro Leu Ser 210 220

Glu Glu Glu Gln Lys Leu Ala Arg Pro Lys Leu Phe Trp Trp Asn Val 225 230 235 240

Leu Leu Phe Leu Ala Ala Met Ser Leu Leu Phe Ser Gly Ile Phe Pro 245 250 255

Pro Gly Tyr Val Phe Met Leu Ala Ala Thr Ala Ala Leu Leu Leu Asn 260 265 270

Tyr Arg Ser Pro Gln Glu Gln Met Glu Arg Ile Tyr Ala His Ala Gly 275 280 285

Gly Ala Val Met Met Ala Ser Ile Ile Leu Ala Ala Gly Thr Phe Leu 290 295 300

Gly Ile Leu Lys Gly Ala Gly Met Leu Asp Ala Ile Ser Lys Asp Ile 305 310 315 320

Val His Ile Leu Pro Asp Ala Leu Leu Pro Tyr Leu His Ile Ala Ile 325 330 335

Gly Val Leu Gly Ile Pro Leu Glu Leu Val Leu Ser Thr Asp Ala Tyr 340 345 350

Tyr Phe Gly Leu Phe Pro Ile Val Glu Glr Ile Thr Ser Gin Ala Gly 355 360 365

Val Ala Pro Glu Ala Ala Gly Tyr Ala Met Leu Ile Gly Ser Ile Val 370 375 380

Gly Thr Phe Val Thr Pro Leu Ser Pro Ala Leu Trp Met Gly Leu Gly 385 390 395 400

Leu Ala Lys Leu Ser Met Gly Lys His Ile Arg Tyr Ser Phe Phe Trp
405 410 415

Ala Trp Gly Leu Ser Leu Ala Ile Leu Ala Ser Ser Ile Ala Ala Gly
420 425

Ile Val Pro Leu Pro 435

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<212> DNA

<213> Neisseria meningitidis

<220>

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act tat Thr Tyr	ctg	tat Tyr 20	caa Gln	aag Lys	ccc Pro	aag Lys	ctc Leu 25	ttt Phe	aaa Lys	gga Gly	gcg Ala	gtt Val 30	cgg Arg	aat Asn	96
ctc gaa Leu Glu	gcc Ala 35	gca Ala	tct Ser	tgt Cys	aaa Lys	tat Tyr 40	atc Ile	aac Asn	gag Glu	ata Ile	tac Tyr 45	caa Gln	cga Arg	gca Ala	144
gac cca Asp Pro	Thr	gca Ala	ccg Pro	ctg Leu	ttt Phe 55	cat His	ctg Leu	cgt Arg	aaa Lys	aaa Lys 60	ggc Gly	gca Ala	atc Ile	gtt Val	192
cct aaa Pro Lys 65	gaa Glu	gaa Glu	tac Tyr	gtc Val 70	gaa Glu	agt Ser	ttc Phe	gac Asp	gat Asp 75	ttg Leu	ggc Gly	aaa Lys	act Thr	cgc Arg 80	240
tac egt Tyr Arg	ttt Phe	att Ile	aaa Lys 85	tcc Ser	gtt Val	atc Ile	tac Tyr	gaa Glu 90	cat His	atg Met	aag Lys	aat Asn	ggt Gly 95	gcg Ala	288
tog tta Ser Lea															336
gcc cg Ala Ar		Val													384
tat ct Tyr Le	: Ala														432
cgc ga Arg As 145															480
act gc Thr Al															528
act ga Thr As			Ile												576
gca gg Ala Gl		Val													624
ccg ct Pro Le 21	u Gly														672
aac gg Asn Gl 225					Glu					Lys					720
gaa ag Glu Se															768

245 250 255

atc Ile	aac Asn	gat Asp	act Thr 260	gcc Ala	gca Ala	caa Gln	att Ile	gct Ala 265	gcc Ala	atg Met	att Ile	gcc Ala	gac Asp 270	ccc Pro	gtc Val	816
aat Asn	tac Tyr	gaa Glu 275	gcc Ala	ttc Phe	agt Ser	gaa Glu	gac Asp 280	ttc Phe	ctc Leu	ggc Gly	aaa Lys	gaa Glu 285	cgc Arg	acc Thr	gat Asp	864
acc Thr	gct Ala 290	ttr Phe	cat His	ctc Leu	gaa Glu	cag Gln 295	ttc Phe	gcg Ala	aat Asn	ccc Pro	aac Asn 300	gct Ala	act Thr	ccg Pro	ctt Leu	912
tca Ser 305	gac Asp	gac Asp	gtc Val	agg Arg	tig Leu 310	aga Arg	cta Leu	aat Asn	gcc Ala	aat Asn 315	aat Asn	ttg Leu	gat Asp	acg Thr	ttg Leu 320	960
gaa Glu	aag	gga Gly	tat Tyr	ttg Leu 325	att Ile	ggg	aat Asn	gjy āgā	atg Met 330	aag Lys	ata Ile	agc Ser	gta Val	gat Asp 335	gaa Glu	1008
ttg Leu	ggg ggg	aaa Lys	aaa Lys 340	gtg Val	tta Leu	gaa Glu	cac	atc Ile 345	ggt Gly	aag Lys	aat Asn	gaa Glu	ecg Pro 350	tta Leu	ttg Leu	1056
ttg Leu	aaa Lys	aat Asn 355	Leu	ctg Leu	gtt Val	aac Asn	ttc Phe 360	aat Asn	cag Gln	gga	aaa Lys	cat His 365	gaa Glu	gaa Glu	gtt Val	1104
agg Arg	aag Lys 370	Leu	att Ile	tat Tyr	cag Gln	ttg Leu 375	Ile	gag Glu	tta Leu	gat Asp	rtt Phe 380	Leu	gaa Glu	ctt Leu	ttg Leu	1152
tga																1155

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<211> 384

<212> PRT

<213> Neisseria meningitidis

<400> 14

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Thr Tyr Leu Tyr Gln Lys Pro Lys Leu Phe Lys Gly Ala Val Arg Asn 20 25 30

Asp Pro Thr Ala Pro Leu Phe His Leu Arg Lys Lys Gly Ala Ile Val 50 60

Pro Lys Glu Glu Tyr Val Glu Ser Phe Asp Asp Leu Gly Lys Thr Arg 65 70 75

Tyr Arg Phe Ile Lys Ser Val Ile Tyr Glu His Met Lys Asn Gly Ala

- Ser Leu Val Tyr Asn His Ile Asn Asn Glu Pro Phe Ser Asp His Ile 100 105 110
- Ala Arg Gln Val Ala Arg Phe Ala Gly Ala His Thr Ile Val Ser Gly 115 120 125
- Tyr Leu Ala Phe Gly Ser Asp Glu Ser Tyr Lys Asn His Trp Asp Thr 130 135 140
- Arg Asp Val Tyr Ala Ile Gln Leu Phe Gly Lys Lys Arg Trp Gln Leu 145 150 155
- Thr Ala Pro Asp Phe Pro Met Pro Leu Tyr Met Gln Gln Thr Lys Asp 165 170 175
- Thr Asp Ile Ser Ile Pro Glu His Ile Asp Met Asp Ile Ile Leu Glu 180 185
- Ala Gly Asp Val Leu Tyr Ile Pro Arg Gly Trp Trp His Arg Pro Ile 195 200 205
- Pro Leu Gly Cys Glu Thr Phe His Phe Ala Val Gly Thr Phe Pro Pro 210 215 220
- Asn Gly Tyr Asn Tyr Leu Glu Trp Leu Met Lys Lys Phe Pro Thr Ile 225 230 235 240
- Glu Ser Leu Arg His Ser Phe Ser Asp Trp Glu Gln Asp Arg Thr Arg 245 250 255
- Ile Asn Asp Thr Ala Ala Gln Ile Ala Ala Met Ile Ala Asp Pro Val 260 255 270
- Asn Tyr Glu Ala Phe Ser Glu Asp Phe Leu Gly Lys Glu Arg Thr Asp 275 280 285
- Thr Ala Phe His Leu Glu Gln Phe Ala Asn Pro Asn Ala Thr Pro Leu 290 295 300
- Ser Asp Asp Val Arg Leu Arg Leu Asn Ala Asn Asn Leu Asp Thr Leu 305 310 315 320
- Glu Lys Gly Tyr Leu Ile Gly Asn Gly Met Lys Ile Ser Val Asp Glu 325 330 335
- Leu Gly Lys Lys Val Leu Glu Hıs Tle Gly Lys Asn Glu Pro Leu Leu 340 345 350
- Leu Lys Asn Leu Leu Val Asn Phe Asn Gln Gly Lys His Glu Glu Val 355 360 365
- Arg Lys Leu Ile Tyr Gln Leu Ile Glu Leu Asp Phe Leu Glu Leu Leu 370 375 380
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- <212> DNA
- <213> Neisseria meningitidis

<221> CDS

<222> (1)..(714)

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Arg Cgc	caa Gln	acc Thr	agc Ser 20	ctg Leu	acg Thr	ggt Gly	aaa Lys	gtg Val 25	att Ile	ctg Leu	aca Thr	cga Arg	ccg Pro 30	ttg Leu	tca Ser	96
ttt Phe	tcc Ser	cta Leu 35	tgg Trp	acg Thr	aca Thr	ttt Phe	gca Ala 40	tcg Ser	ata Ile	tct Ser	gcg Ala	tta Leu 45	ttg Leu	att Ile	atc Ile	144
ctg Leu	ttt Phe 50	ttg Leu	ata Ile	ttt Phe	ggt Gly	aac Asn 55	tat Tyr	acg Thr	cga Arg	aag Lys	aca Thr 60	aca Thr	gtg Val	gag Glu	gga Gly	192
caa Gln 65	att Ile	tta Leu	cct Pro	gca Ala	tcg Ser 70	ggc Gly	gta Val	atc Ile	agg Arg	gtg Val 75	tat Tyr	gca Ala	ccg Pro	gat Asp	acg Thr 80	240
				gcg Ala 85												288
	-	_		ttt Phe			-			_			_		_	336
				cag Gln												384
		_	_	ctg Leu		_	_	_								432
_	Ser			gca Ala			-	_								480
				ata Ile 165						Arg						528
				aaa Lys										Val		576
			Met	atg Met				Ala					Gln			624
			_	tac Tyr	_	_	_	_	_			Leu			atc 1 Ile	672
cgc Arg 225	acg Thr	cag Gln	aat Asn	ctg Leu	aca Thr 230	ttg Leu	gcc Ala	agc Ser	ctc Leu	ecc Pro 235	Gln	gcg Ala	gca Ala	tga t	a	717

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- <211> 238
- <212> PRT
- <213> Neisseria meningitidis

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Phe Ser Leu Trp Thr Thr Phe Ala Ser Ile Ser Ala Leu Leu Ile Ile 35 40 45

Leu Phe Leu Ile Phe Gly Asn Tyr Thr Arg Lys Thr Thr Val Glu Gly 50 60

Gln Ile Leu Pro Ala Ser Gly Val Ile Arg Val Tyr Ala Pro Asp Thr 65 70 75 80

Gly Thr Ile Thr Ala Lys Phe Val Glu Asp Gly Glu Lys Val Lys Ala 85 90 95

Gly Asp Lys Leu Phe Ala Leu Ser Thr Ser Arg Phe Gly Ala Gly Asp 100 105 110

Ser Val Gln Gln Leu Lys Thr Glu Ala Val Leu Lys Lys Thr Leu 115 120 125

Ala Glu Glu Leu Gly Arg Leu Lys Leu Ile His Gly Asn Glu Thr 130 140

Arg Ser Leu Lys Ala Thr Val Glu Arg Leu Glu Asn Gln Lys Leu His 145 150 155 160

Ile Ser Gln Gln Ile Asp Gly Gln Lys Arg Arg Ile Arg Leu Ala Glu 165 170 175

Glu Met Leu Gln Lys Tyr Arg Phe Leu Ser Ala Asn Asp Ala Val Pro 180 185 190

Lys Gln Glu Met Met Asn Val Lys Ala Glu Leu Leu Glu Gln Lys Ala 195 200 205

Lys Leu Asp Ala Tyr Arg Arg Glu Glu Val Gly Leu Leu Gln Glu Ile 210 . 215 220

Arg Thr Gln Asn Leu Thr Leu Ala Ser Leu Pro Gln Ala Ala 225 230 235

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<213> Neisseria meningitidis

<220>

<221> CDS

<222> (1)..(687)

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gcc Ala	tac Tyr	ggc Gly	cga Arg 20	gaa Glu	gaa Glu	gcc Ala	gly ggg	ctg Leu 2 5	ctt Leu	cag Gln	gaa Glu	atc Ile	cgc Arg 30	acg Thr	cag Gln	96
aat Asn	ctg Leu	aca Thr 35	ttg Leu	gcc Ala	agc Ser	ctc Leu	ccc Pro 40	aaa Lys	cgg Arg	cat His	gag Glu	aca Thr 45	gaa Glu	caa Gln	agc Ser	144
cag Gln	ctt Leu 50	gaa Glu	c gc Arg	acc Thr	atg Met	gcc Ala 55	gat Asp	att Ile	tct Ser	caa Gln	gaa Glu 60	gtt Val	ttg Leu	gat Asp	ttt Phe	192
gaa Glu 65	atg Met	cgc Arg	tct Ser	gaa Glu	caa Gln 70	atc Ile	atc Ile	cgt Arg	gca Ala	gga Gly 75	cgg Arg	tcg Ser	ggt Gly	tat Tyr	ata Ile 80	240
gca Ala	ata Ile	ccg Pro	aac Asn	gtc Val 85	gaa Glu	gtc Val	gga Gly	cag Gln	cag Gln 90	gtt Val	gat Asp	cct Pro	tcc Ser	aaa Lys 95	ctg Leu	288
ctc Leu	ttg Leu	agc Ser	att Ile 100	gtt Val	ccc Pro	gaa Glu	egt Arg	acc Thr 105	gag Glu	cta Leu	tat Tyr	gcc Ala	cat His 110	cta Leu	tat Tyr	336
atc Ile	ccc Pro	agc Ser 115	Ser	gca Ala	gca Ala	ggc Gly	ttt Phe 120	Ile	aag Lys	ccg Pro	aaa Lys	gac Asp 125	aag Lys	gtt Val	gtc Val	384
cta Leu	cgt Arg 130	Туг	cag Gln	gca Ala	tat Tyr	ccc Pro 135	Tyr	caa Gln	aaa Lys	ttc Phe	ggg Gly 140	Leu	gct Ala	tcc Ser	ggc	432
agt Ser 145	Val	gta Val	tça Ser	gta Val	gca Ala 150	Lys	acg Thr	gca Ala	ctg Leu	gg Gl _y 155	/ Arg	cag Glr	gaa Glu	ttg Lev	tcg Ser 160	480
gga Gly	ttg Lev	ggo Gly	atg Met	gta Val		tcc Ser	gat Asp	ttg Lev	g gcg 1 Ala 170	ı Lys	g ago s Ser	: aac : Ası	gaa Glu	oct Pro 175) Val	528
tat Tyr	cto Lev	gtg 1 Val	g aaa L Lys 180	: Ile	a aaa e Lys	ccc Pro	gac Asp	aaa Lys 189	Pro	a aco	e ato	e act	gca Ala 190	ı Tyr	ggt Gly	576
gag	gaa	a aaa	a cca	g cts	g caa	ato	999	ate	gac	g tr	g gaa	a gca	a ga	ato	ctg	624
			Pro					Met					Asp		Leu	
cac His	gag Glu 210	. Lys	. cgg . Arg	cgg	ctg Leu	tac Tyr 215	Glu	tgg Trp	gta Val	ttg Lei	g gag 2 Glu 220	Lue	att Ile	tat Tyr	agt Ser	672
_		_	aaa Lys		taa	L				٠						690

- <210> 18
- <211> 229
- <212> PRT
- <213> Neisseria meningitidis

<400> 18

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Ala Tyr Gly Arg Glu Glu Ala Gly Leu Leu Gln Glu Ile Arg Thr Gln 20 25 30

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Gln Leu Glu Arg Thr Met Ala Asp Ile Ser Gln Glu Val Leu Asp Phe 50 60

Glu Met Arg Ser Glu Gln Ile Ile Arg Ala Gly Arg Ser Gly Tyr Ile 65 70 75 80

Ala Ile Pro Asn Val Glu Val Gly Gln Val Asp Pro Ser Lys Leu 85 90 95

Leu Leu Ser Ile Val Pro Glu Arg Thr Glu Leu Tyr Ala His Leu Tyr 100 105 110

Ile Pro Ser Ser Ala Ala Gly Phe Ile Lys Pro Lys Asp Lys Val Val 115 120 125

Leu Arg Tyr Gln Ala Tyr Pro Tyr Gln Lys Phe Gly Leu Ala Ser Gly 130 140

Ser Val Val Ser Val Ala Lys Thr Ala Leu Gly Arg Gln Glu Leu Ser 145 150 155

Gly Leu Gly Met Val Ser Ser Asp Leu Ala Lys Ser Asn Glu Pro Val 165 170 175

Tyr Leu Val Lys Ile Lys Pro Asp Lys Pro Thr Ile Thr Ala Tyr Gly 180 185 190

Glu Glu Lys Pro Leu Gln Ile Gly Met Thr Leu Glu Ala Asp Ile Leu 195 200 205

His Glu Lys Arg Arg Leu Tyr Glu Trp Val Leu Glu Leu Ile Tyr Ser 210 215 220

Met Ser Gly Lys Leu 225

<210> 19

<211> 1743

<212> DNA

<213> Neisseria meningitidis

<220>

<221> CDS

<222> (1)..(1740)

<400)> 19)														
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1				5					10					15		
					_	-	_	gaa		-	-	-			-	96
Pro	Leu	Lys		Leu	Ala	Ala	Asp	Glu	Asn	Asp	Ala	Glu		Ile	Arg	
			20					25					30			
	a + ~	~~~		~~~	a 3 a	C 2 C	242	gat	~~+	~==	+	++=	200	ant.	acs.	144
	_	_	_	-	_			Asp	-	_	_			_	_	177
00		35	AT 9	GIII	0111	11.4.4	40	7100		,		45		пор	7124	
aat	gtc	cgt	ttc	gag	caa	cca	ttg	gag	aag	aac	aat	tat	gtc	ctg	agt	192
								Glu								
	50					55					60					
_		_		_	_			gta				_		-	-	240
65	ASD	Gill	inr	Pro	-	Thr	Arg	Val	ASI	75	TTE	ser	ren	Asp	Asp 80	
3.5					70					,5					80	
aaq	ac=	aca	cac	222	ttt	tat	ttt	ctt	cct	tct	ata	ctc	ato	aaa	caa	288
								Leu								
-				85					90					95		
								tta								336
Thr	Ala	Phe		Thr	Gly	Met	Cys	Leu	Gly	Ser	Asn	Asn		Ser	Arg	
			100					105					110			
CT a	~==	227	~~~	~~~	~			a+ ~		~+ ~	~~+		+			384
								ctg Leu								204
	22	115		Ald	0111	0111	120				J	125	- 1 -	2400	****	
tcc	caa	gct	att	atc	caa	cca	cag	aat	atg	gat	tog	gga	att	ctg	aaa	432
Ser	Gln	Ala	Ile	Ile	Gln	Pro	Gln	Asn	Met	Asp	Ser	Gly	Ile	Leu	Lys	
	130					135					140					
tta	cgg	gta	tca	gca	ggc	gaa	atc	agg	gat	atc	cgc	tat	gaa	gaa	aaa	480
145	Arg	Val	ser	Ala		Glu	Ile	Arg	Asp		Arg	Tyr	Glu	GLu		
7.7.					150					155					160	
cga	gat	aca	aao	tat	acc	gag	aac	agt	att	agt	qca	ttc	aat	aac	aaa	528
								Ser								
_	-		•	165			_		170					175	• -	
								•								
ctt	ccc	tta	tat	agg	aac	aaa	att	ctc	aat	ctt	cgc	gat	gta	gag	cag	576

Leu	Pro	Leu	Tyr 180	Arg	Asn	Lys	ile	Leu 185	Asn	Leu	Arg	Asp	Val 190	Glu	Gln	
ggc Gly	ttg Leu	gaa Glu 195	aac Asn	ctg Leu	cgt Arg	cgt Arg	ttg Leu 200	ccg Pro	agt Ser	gtt Val	aaa Lys	aca Thr 205	gat Asp	att Ile	cag Gln	624
att Ile	ata Ile 210	ccg Pro	tcc Ser	gaa Glu	gaa Glu	gaa Glu 215	ggc Gly	aaa Lys	agc Ser	gat Asp	tta Leu 220	cag Gln	atc Ile	aaa Lys	tgg Trp	672
cag Gln 225	cag Gln	aat Asn	aaa Lys	ccc Pro	ata Ile 230	cgg	ttc Phe	agt Ser	atc Ile	ggt Gly 235	ata Ile	gat Asp	gat Asp	gcg Ala	ggc Gly 240	720
Gjà	aaa Lys	acg Thr	acc Thr	ggc Gly 245	aaa Lys	tat Tyr	caa Gln	gga Gly	aat Asn 250	gtc Val	gct Ala	tta Leu	tcg Ser	tcc Ser 255	gat Asp	768
aac Asn	cct Pro	ttg Leu	99c Gly 260	tta Leu	agc Ser	gat Asp	tcg Ser	ttt Phe 265	tat Tyr	gtt Val	tca Ser	tat Tyr	gga Gly 270	cgc Arg	ggr	816
ttg Leu	gtg Val	cac His 275	Lys	acg Thr	gac Asp	ttg Leu	act Thr 280	gct Ala	gcc Ala	acc Thr	ggt Gly	acg Thr 285	gaa Glu	act Thr	gaa Glu	864
agc Ser	gga Gly 290	Ser	aga Arg	agt Ser	tac Tyr	agc Ser 295	Val	cat H1s	tat Tyr	tcg Ser	gtg Val 300	ccc Pro	gta Val	aaa Lys	aaa Lys	912
tgg Trp 305	Lev	ttt Phe	tct Ser	ttt Phe	aat Asn 310	. His	aat Asn	gga Gly	cat	. cgt Arg 315	Tyr	cac His	gaa Glu	gca Ala	acc Thr 320	960
gaa Glu	ggo Gly	tat Tyr	too Ser	gto Val	. Asr	tac Tyr	gat Asp	tac Tyr	aac Asr 330	ı Gly	aaa Lys	caa Gln	tat Tyr	cag Gln 335	. Ser	1008
ago Ser	cto	g gcc 1 Ala	gco A Ala 340	a Gli	g ogo 1 Arg	atg Met	; ctt : Lev	tgg Trp 345	Pro	ccc Pro	ago Sei	ttt Phe	cct Pro 350	Glr	act Thr	1056
tca Ser	gto Val	c cga l Arg 359	g Met	g aaa Lys	a tta s Lei	tgg Trp	g aca Thi	: Arg	caa g Gli	a acc	c tat	aaa Lys 365	Tyr	ato Ile	gac Asp	1104
gat	gco Ala 37	a Glu	a ato 1 Ile	gaa e Glu	a gtg ı Val	g caa L Glr 375	n Arg	c cgo g Aro	g Ar	c tc: g Se:	r gca r Ala 38	a Gly	tgg Tr <u>p</u>	gaa Glu	a gcc ı Ala	1152
gaa Glu 38	ı Le	g cgo	cac g Hi	c cg	t got g Ala 39	a Ty:	c cto	c cad i Hi:	c cg	t tg g Tr 39	p Gl:	g cti n Lei	gad 1 Asp	gg Gl	aag Y Lys 400	1200
tt: Le:	g tc ı Se	t tad	c aa r Ly	a cg s Ar 40	g Gl	g aco	c gg r Gl	c at y Me	g cg t Ar 41	g Gl	a ag n Se	t ate	g cco	gc. Al:	a cct a Pro 5	1248
ga	a ga	a aa	c gg	c gg	c gg	t ac	t at	t cc	a gc	c ac	a tc	c cg	t at	g aa	a atc	1296

	Glu	Glu	Asn	Gly 420	Gly	Gly	Thr	Ile	Pro 425	Ala	Thr	Ser	Arg	Met 430	Lys	Ile	
									gcc Ala								1344
									caa Gln								1392
									atc Ile								1440
									ttc Phe								1488
									cat His 505								1536
									ggc Gly								1584
									gtc Val								1632
									ctg Leu								1680
									aac Asn								1728
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<212> PRT

<213> Neisseria meningitidis

<400> 20

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Pro Leu Lys Thr Léu Ala Ala Asp Glu Asn Asp Ala Glu Leu Ile Arg

Ser Met Gln Arg Gln Gln His Ile Asp Ala Glu Leu Leu Thr Asp Ala 40

Asn Val Arg Phe Glu Gln Pro Leu Glu Lys Asn Asn Tyr Val Leu Ser

- Glu Asp Glu Thr Pro Cys Thr Arg Val Asn Tyr Ile Ser Leu Asp Asp 65 70 75 80
- Lys Thr Ala Arg Lys Phe Ser Phe Leu Pro Ser Val Leu Met Lys Glu 90 95
- Thr Ala Phe Lys Thr Gly Met Cys Leu Gly Ser Asn Asn Leu Ser Arg
- Leu Gln Lys Ala Ala Gln Gln Ile Leu Ile Val Arg Gly Tyr Leu Thr
- Ser Gln Ala Ile Ile Gln Pro Gln Asn Met Asp Ser Gly Ile Leu Lys 130 135 140
- Leu Arg Val Ser Ala Gly Glu Ile Arg Asp Ile Arg Tyr Glu Glu Lys
 145 150 155 160
- Arg Asp Ala Lys Ser Ala Glu Gly Ser Ile Ser Ala Phe Asn Asn Lys 165 170 175
- Leu Pro Leu Tyr Arg Asn Lys Ile Leu Asn Leu Arg Asp Val Glu Gln
 180 185 190
- Gly Leu Glu Asn Leu Arg Arg Leu Pro Ser Val Lys Thr Asp Ile Gln 195 200 205
- Ile Ile Pro Ser Glu Glu Glu Gly Lys Ser Asp Leu Gln Ile Lys Trp 210 215 220
- Gln Gln Asn Lys Pro Ile Arg Phe Ser Ile Gly Ile Asp Asp Ala Gly 225 230 235 240
- Gly Lys Thr Thr Gly Lys Tyr Gln Gly Asn Val Ala Leu Ser Ser Asp 245 250 255
- Asn Pro Leu Gly Leu Ser Asp Ser Phe Tyr Val Ser Tyr Gly Arg Gly 260 265 270
- Leu Val His Lys Thr Asp Leu Thr Ala Ala Thr Gly Thr Glu Thr Glu 275 280 285
- Ser Gly Ser Arg Ser Tyr Ser Val His Tyr Ser Val Pro Val Lys Lys 290 295 300
- Trp Leu Phe Ser Phe Asn His Asn Gly His Arg Tyr His Glu Ala Thr 305 310 315 320
- Glu Gly Tyr Ser Val Asn Tyr Asp Tyr Asn Gly Lys Gln Tyr Gln Ser 325 330 335
- Ser Leu Ala Ala Glu Arg Met Leu Trp Pro Pro Ser Phe Pro Gln Thr
- Ser Val Arg Met Lys Leu Trp Thr Arg Gln Thr Tyr Lys Tyr Ile Asp 355 360 365
- Asp Ala Glu Ile Glu Val Gln Arg Arg Ser Ala Gly Trp Glu Ala

The first first the first give first
m

370

375 .

380

Glu Leu Arg His Arg Ala Tyr Leu His Arg Trp Gln Leu Asp Gly Lys 385 390 395 400

Leu Ser Tyr Lys Arg Gly Thr Gly Met Arg Gln Ser Met Pro Ala Pro 405 410 415

Glu Glu Asn Gly Gly Gly Thr Ile Pro Ala Thr Ser Arg Met Lys Ile 420 425 430

Ile Thr Ala Gly Leu Asp Ala Ala Pro Ser Met Leu Gly Lys Gln $435 \ \ \, 440 \ \ \, 445$

Gln Phe Phe Tyr Ala Thr Ala Ile Gln Ala Gln Trp Asn Lys Thr Pro $450 \hspace{1cm} 455 \hspace{1cm} 460$

Leu Val Ala Gln Asp Lys Leu Ser Ile Gly Ser Arg Tyr Thr Val Arg 465 470 475 480

Gly Phe Asp Gly Glu Gln Ser Leu Phe Gly Glu Arg Gly Phe Tyr Trp 485 490 495

Gln Asn Thr Leu Thr Trp Tyr Phe His Pro Asn His Gln Phe Tyr Leu 500 505 510

Gly Ala Asp Tyr Gly Arg Val Ser Gly Glu Ser Ala Gln Tyr Val Ser 515 520 525

Gly Lys Gln Leu Met Gly Ala Val Val Gly Phe Arg Gly Gly His Lys 530 540

Val Gly Gly Met Phe Ala Tyr Asp Leu Phe Ala Gly Lys Pro Leu His 545 550 555

Lys Pro Lys Gly Phe Gln Thr Thr Asn Thr Val Tyr Gly Phe Asn Leu 565 570 575

Asn Tyr Ser Phe 580

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<211> 411

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<213> Neisseria meningitidis

<220>

<221> CDS

<222> (1)..(408)

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															s Ala	
			20					25					3 (0		
gaa	aca	aaa	caa	acc	acc	cta	att	acc	acc	tat	cqq	cat	tct	tct	atg	144
Glu	Ala	Lys	Gln	Thr	Ala	Leu	Ile	Ãla	Thr	Tyr	Arg	His	Ser	Ser	Met	
		35					40					45				
gtt	gcg	gcg	gaa	caa	tac	gcc	ttg	cag	ctt	aaa	aaa	gcg	cag	gac	gaa	192
Val	Ala 50	Ala	Glu	Gln	Tyr	Ala 55	Leu	GIN	ьeu	гуя	_ р у	Ala	GIII	Asp	G2 L	
													224	050	ata	240
agg Arg	cag Gln	cgg Arg	tgg Trp	tac Tyr	gac Asp	Phe	ser	Gln	Lys	Gln	Gly	Arg	Lys	Pro	Val	240
65		-			70					75					80	
aaa	aaa	cag	tat	ccg	ccg	caa	acg	aaa	aaa	gcc	ggc	tat	ctg	aaa	acc	288
Lys	Lys	Gln	Tyr	Pro 85	Pro	Gln	Thr	Lys	Lys 90	Ala	Gly	Tyr	Leu	Lys 95	Thr	
														-		
aag	gaa	gaa	ctg	ctt Leu	gcg	gaa	ttg	gct Ala	tgc	Ctt	aaa Lvs	gcg Ala	gaa Glu	atg Met	gct Ala	336
נעב		GIG	100	ine u	AIG	G1.4		105	-7-				110			
acc	cta	222	220	ctc	gat	acc	tta	atc	tat	ada	aaa	qaa	ata	cgq	cag	384
Ala	Leu	Lys	Lys	Leu	Asp	Ala	Leu	Ile	Tyr	ĞÎy	Lys	Glu	Val	Arg	Gln	
		115					120					125				
				tcg												411
глу	G1U		Asn	Ser	ser	135	GTÅ									

<210> 22

<211> 136

<212> PRT

<213> Neisseria meningitidis

<400> 22

Met Ile Glu Phe Val Arg Ala Lys Lys Arg Leu Leu Trp Ala Phe Val 1 5 10 15

Leu Leu Leu Val Trp Thr Cys Gly Tyr Arg Tyr Ala Ala Asp Lys Ala 20 25 30

Glu Ala Lys Gln Thr Ala Leu Ile Ala Thr Tyr Arg His Ser Ser Met 35 40 45

Val Ala Ala Glu Gln Tyr Ala Leu Gln Leu Lys Lys Ala Gln Asp Glu 50 55 60

Arg Gln Arg Trp Tyr Asp Phe Ser Gln Lys Gln Gly Arg Lys Pro Val 65 70 75 80

Lys Lys Gln Tyr Pro Pro Gln Thr Lys Lys Ala Gly Tyr Leu Lys Thr 85 90 95

Lys Glu Glu Leu Ala Glu Leu Ala Cys Leu Lys Ala Glu Met Ala
100 105 110

Ala Leu Lys Lys Leu Asp Ala Leu Ile Tyr Gly Lys Glu Val Arg Gln 115 120 125

Lys Glu Arg Asn Ser Ser Gln Gly 130

<210> 23

<211> 924

<212> DNA

<213> Neisseria meningitidis

<220>

<221> CDS

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tca gg Ser Gl	y Arg														192
tcc gt Ser Va 65															240
gtg cg Val Ar	_	_					_	_		_	_	_			288
ttt gg Phe Gl															336
aaa tt Lys Le															384
ttc at Phe Il 13	e Thr	ctc Leu	ccg Pro	ttg Leu	ttg Leu 135	ege Arg	gcc Ala	cac His	gcc Ala	cgc Arg 140	tat Tyr	ttc Phe	ggc Gly	aaa Lys	432
ctc gc Leu Al 145	a ctg a Leu	att Ile	cat Hís	ttt Phe 150	gac Asp	gcg Ala	cac His	acc Thr	gac Asp 155	acc Thr	tac Tyr	gac Asp	aac Asn	ggc Gly 160	480
agc ga Ser Gl															528
ctc at	c gac	ccg	tcc	cgt	tcc	gta	caa	atc	ggc	ata	cgt	acc	gaa	cac	576

Leu	Ile	Asp	Pro 180	Ser	Arg	Ser	Val	Gln 185	Ile	Gly	·Ile	Arg	Thr 190	Glu	His	
											ccc Pro					624
											gaa Glu 220					672
	Pro	-		_			-		-		ctc Leu	_	_	_		720
										Gly	ttg Leu					768
											gac Asp					816
		-	_	~	_						tcc Ser	_			_	864
											tac Tyr 300					912
_	Lys	gac Asp	tga													924
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Asn	Asn	Phe	Gly 20		e Le	u Ar	g Le	eu P	ro : 25	Leu	Asn	Phe	Met	Pro 30	Tyr	Glu
Ser	His	Ala 35	Asp	Trp	v Val	1 [1		nr G 10	ly '	Val	Pro	Tyr	Asp 45	Met	Ala	Val
	50					5	55					60			Arg	
Ser 65	Val	Asń	Leu	Ala	7 Tr		u H	is A	rg .	Arg	Phe 75	Pro	Trp	Thr	Phe	Asp 80

Val Arg Glu Arg Leu Asn Ile Ile Asp Cys Gly Asp Leu Val Phe Ser 85 90 95 Phe Gly Asp Ser Arg Asp Phe Val Glu Lys Met Glu Ala His Ala Gly 100 105 110

Lys Leu Leu Ser Ser Gly Lys Arg Cys Leu Ser Leu Gly Gly Asp His 115 120 125

Phe Ile Thr Leu Pro Leu Leu Arg Ala His Ala Arg Tyr Phe Gly Lys 130 135 140

Leu Ala Leu Ile His Phe Asp Ala His Thr Asp Thr Tyr Asp Asn Gly 145 150 160

Ser Glu Tyr Asp His Gly Thr Met Phe Tyr Thr Ala Pro Lys Glu Gly 165 170 175

Leu Ile Asp Pro Ser Arg Ser Val Gln Ile Gly Ile Arg Thr Glu His
180 . 185 190

Ser Lys Lys Leu Pro Phe Thr Val Leu Thr Ala Pro Gln Val Asn Glu 195 200 205

Asp Ser Val Glu Glu Thr Val Arg Lys Ile Lys Glu Thr Val Gly Asn 210 215 220

Met Pro Val Tyr Leu Thr Phe Asp Ile Asp Cys Leu Asp Pro Ser Phe 225 230 235 240

Ala Pro Gly Thr Gly Thr Pro Val Cys Gly Gly Leu Ser Ser Asp Arg 245 250 255

Ala Leu Lys Ile Leu Arg Gly Leu Thr Asp Leu Asp Ile Val Gly Met 260 265 270

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Leu Ala Gly Ala Thr Ile Ala Leu Glu Met Leu Tyr Leu Gln Gly Ala 290 295 300

Lys Lys Asp 305

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<212> DNA

<213> Neisseria meningitidis

<220>

<221> CDS

<222> (1)..(423)

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					aaa Lys											48
					acc Thr											96
					tgc Cys											144
		Tyr			acc Thr											192
-	Trp			-	Pro	Cys			_	_				_	_	240
					gca Ala											288
				Val	gca Ala		-		Ser	_	_		_	-		336
			Āla		gac Asp			_	_							384
	_	Pro			cgt Arg		_		-			Ala	taa			426

<210> 26

<211> 141

<212> PRT

<213> Neisseria meningitidis

<400> 26

Met Glu Gln Ser Gly Lys Phe Ser Trp Ser Ala Ala Ala Phe Trp Asp 1 5 10

Ile Pro Tyr Pro Val Thr Arg Arg Ile Ala Ser Ser Leu Tyr Ser Thr 20 25 30

Glu Tyr Phe Val Val Cys Phe Leu Arg Leu Met Pro Leu Ser Pro Cys
35 40 45

Asn Leu Tyr Phe Val Thr His Leu Arg Thr Asn Glu Ser Glu Ile Glu 50 55 60

Arg Trp Ser Ala Val Pro Cys Gln Ile Val Leu Asn Asp Gly Lys Ser 65 70 75 80

Glu Phe Gly Gly Phe Ala Phe Glu Val Gln Leu Ser Leu Thr Glu Lys
85 90 95

Gly Gln Tyr Ala Val Ala Tyr Asp Leu Ser Cys Lys Lys Asp Cys His

Glu Leu His Ala Thr Asp Pro Arg Arg Thr Ile Pro His Pro Ile Pro 115 120 125

Val Pro Pro Leu His Arg His Arg Asn Arg Gln Thr Ala 130 135 140

<210> 27

<211> 351

<212> DNA

<213> Neisseria meningitidis

<220>

<221> CDS

<222> (1)..(348)

<40	0 > 21	7												
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- : -	att Ile	_	-	_	_		-		 -	_	_	_		96
	aaa Lys		_	-	_	_		_			_		_	144
	ggc Gly 50													192
_	tac Tyr	_			-	_	_				_			240
	tat Tyr				~		~							288
	ccc Pro													336
	cgc Arg			tga										351

<210> 28

<211> 116

<212> PRT

<213> Neisseria meningitidis

<400> 28

Met Gln Asn Gly Gly Gly Lys Ile Tyr Gln Thr Ala Asp Asn Val Glu 1 5 10 15

Gly Ile Met Leu Lys Val Val Pro Glu Arg Thr Val Ser Ala Asp

Ala Lys Thr Arg Asp Pro Met Trp Asp Asn Ala Ala Leu Gln Thr Ser 35 40 45

Glu Gly Val Asn Phe Ile Ala Arg Phe Leu Gly Phe Phe Ser Asp Gly 50 60

Glu Tyr Arg Tyr Val Asp Val Leu Gln Pro Asn His Ser Asp Ile Ile
65 70 75 80

Arg Tyr Ser Gly Lys Asp Phe Pro Leu Asn Gln Ile Leu Asn His Ile 85 90 95

His Pro Ala Arg Tyr Ala Val Thr Phe Glu Asn Asn Val Asp Ser Lys
100 105 110

Leu Arg Arg His 115

<210> 29

<211> 1404

<212> DNA

<213> Neisseria meningitidis

<220>

<221> CDS

<222> (1)..(1401)

<400> 29

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Met Thr Leu Leu Asn Leu Met Ile Met Gln Asp Tyr Gly Ile Ser Val

1 5 10 15

tgc ctg aca ctg acg ccc tat ttg caa cat gaa cta ttt tcg gct atg 96 Cys Leu Thr Leu Thr Pro Tyr Leu Gln His Glu Leu Phe Ser Ala Met

asa too tat tit too asa tat ato ots coo git too cit tit acc tity
Lys Ser Tyr Phe Ser Lys Tyr Ile Leu Pro Val Ser Leu Phe Thr Leu
35 40 45

Pro Leu Ser Leu Ser Pro Ser Val Ser Ala Phe Thr Leu Pro Glu Ala
50 55 60

tgg cgg gcg gcg cag caa cat tcg gct gat ttt caa gcg tcc cat tac 240
Trp Arg Ala Ala Gln Gln His Ser Ala Asp Phe Gln Ala Ser His Tyr
65 70 75 80

cag cgt gat gca gtg cgc gca cgg caa caa caa gcc aag gcc gca ttc 288 Gln Arg Asp Ala Val Arg Ala Arg Gln Gln Gln Ala Lys Ala Ala Phe 85 90 95

ctt ccc cat gta tcc gcc aat gcc agc tac cag cgc cag ccg cca tcg 336 Leu Pro His Val Ser Ala Asn Ala Ser Tyr Gln Arg Gln Pro Pro Ser 100 105 110

att tot toc acc ogo gaa aca cag gga tgg ago gtg cag gtg gga caa 38

Il	e	Ser	Ser 115	Thr	Arg	Glu	Thr	Gln 120	Gly	Trp	Ser	Val	Gln 125	Val	Gly	Gln	
a c	ır	tta Leu 130	ttt Phe	gac Asp	gct Ala	gcc Ala	aaa Lys 135	ttt Phe	gca Ala	caa Gln	tac Tyr	cgc Arg 140	caa Gln	agc Ser	agg Arg	ttc Phe	432
As	at sp	acg Thr	cag Gln	gct Ala	gca Ala	gaa Glu 150	cag Gln	cgt Arg	ttc Phe	gat Asp	gcg Ala 155	gca Ala	cgc Arg	gaa Glu	gaa Glu	ttg Leu 160	480
C1 Le	tg eu	tig Leu	aaa Lys	gtt Val	gcc Ala 165	gaa Glu	agt Ser	tat Tyr	ttc Phe	aac Asn 170	gtt Val	tta Leu	ctc Leu	agc Ser	cga Arg 175	gac Asp	528
a T	cc hr	gtt Val	gcc Ala	gcc Ala 180	cat His	gcg Ala	gcg Ala	gaa Glu	aaa Lys 185	gag Glu	gct Ala	tat Tyr	gcc Ala	cag Gln 190	cag Gln	gta Val	576
a A	gg .rg	cag Gln	gcg Ala 195	Gln	gct Ala	tta Leu	ttc Phe	aat Asn 200	aaa Lys	ggt Gly	gct Ala	gcc Ala	acc Thr 205	gcg Ala	ctg Leu	gat Asp	624
a	tt 1e	cac His 210	Glu	gcc Ala	aaa Lys	gcc Ala	ggt Gly 215	tac Tyr	gac Asp	aat Asn	gcc Ala	ctg Leu 220	Ala	caa Gln	gaa Glu	atc Ile	672
P	scc Ala 225	Val	ttg Lev	gct Ala	gag Glu	aaa Lys 230	caa Gln	acc Thr	tat Tyr	gaa Glu	aac Asn 235	Glr	ttg Leu	aac Asn	gac Asp	tac Tyr 240	720
ī	cc	gac	ctg	gat 1 Asp	agc Ser 245	aaa Lys	çaa Gln	atc Ile	gag Glu	gco Ala 250	Il∈	gat Asp	acc Thr	gcc Ala	aac Asn 255	ьец	768
ţ	teu	gca Ala	e cgo	tat Type 260	: Leu	ccc Pro	aag Lys	ctg Lev	gaa Glu 265	Arc	tac Tyi	agt Set	ctg Lev	gat Asp 270	GIT	tgg Trp	816
(caç Glr	g ego	27!	a Ala	tta a Lev	tcc Ser	aac Asr	aat Asi 280	n His	gaa Glu	a tao	c cg	g ato g Met 28:	: Gl:	g caç n Glr	ctt Leu	864
	gco	c ctq a Le 29	u Gl	a ag n Se	c ago r Sei	gga Gly	cas Glr 295	n Ala	g ctt a Let	. cg	g gc:	a gc a Al 30	a Gli	g aad n Asi	ago n Sei	cgc Arg	912
	tat Ty: 30	r Pr	c ac o Th	c gt r Va	t tci l Se:	gcc r Ala 310	a Hi:	t gt	c ggd	ta Y Ty	t ca r Gl 31	n As	t aa n As:	c cto n Le	tae u Ty:	c act r Thr 320	960
	tc: Se:	a tc r Se	t gc r Al	g ca a Gl	g aa n As: 32	n Ası	c ga n Asj	c ta p Ty	c ca r Hi	c ta s Ty 33	r Ar	g gg g Gl	c aa y Ly	a gg s Gl	g at y Me 33	g agc t Ser 5	1008
	gt Va	c gg 1 Gl	c gt y Va	a ca .1 G1 34	n Le	g aa u As:	t tt n Le	g cc u Pr	g ct o Le 34	и Ту	t ac r Th	c gg r Gl	y Gl	a ga y Gl 35	u Le	g tcg u Ser	1056
	9 9	c aa	a at	c ca	t ga	a gc	c ga	a go	g ca	a ta	.c gg	ia ad	c go	c ga	a go	a cag	1104

Gly Lys Ile His Glu Ala Glu Ala Gln Tyr Gly Ala Ala Glu Ala Gln 355 360 ctg acc gca acc gag cgg cac atc aaa ctc gcc gta cgc cag gct tat Leu Thr Ala Thr Glu Arg His Ile Lys Leu Ala Val Arg Gln Ala Tyr 1200 acc gaa age ggt geg egt tac caa atc atg geg caa gaa egg gtt Thr Glu Ser Gly Ala Ala Arg Tyr Gln Ile Met Ala Gln Glu Arg Val ttg gaa age age egt ttg aaa erg aaa teg ace gaa ace gge caa caa 1248 Leu Glu Ser Ser Arg Leu Lys Leu Lys Ser Thr Glu Thr Gly Gln Gln 405 410 tac ggc atc cgc aac cgg ctg gaa gta ata cgg gcg cgg cag gaa gtc Tyr Gly Ile Arg Asn Arg Leu Glu Val Ile Arg Ala Arg Gln Glu Val 1296 1344 gee caa gea gaa cag aaa etg get caa gea egg tat aaa tte atg etg Ala Gln Ala Glu Gln Lys Leu Ala Gln Ala Arg Tyr Lys Phe Met Leu get tat ttg ege ttg gtg aaa gag age ggg tta ggg ttg gaa acg gta 1392 Ala Tyr Leu Arg Leu Vai Lys Glu Ser Gly Leu Gly Leu Glu Thr Val 455 ttt gcg gaa taa 1404 Phe Ala Glu ÷65

<210> 30

<211> 467

<212> PRT

<213> Neisseria meningitidis

<400> 30

Met Thr Leu Leu Asn Leu Met Ile Met Gln Asp Tyr Gly Ile Ser Val

Cys Leu Thr Leu Thr Pro Tyr Leu Gin His Glu Leu Phe Ser Ala Met 20 25 30

Lys Ser Tyr Phe Ser Lys Tyr Ile Leu Pro Val Ser Leu Phe Thr Leu 35 40 45

Pro Leu Ser Leu Ser Pro Ser Val Ser Ala Phe Thr Leu Pro Glu Ala 50 55 60

Trp Arg Ala Ala Gln Gln His Ser Ala Asp Phe Gln Ala Ser His Tyr 65 70 75 80

Gln Arg Asp Ala Val Arg Ala Arg Gln Gln Ala Lys Ala Ala Phe 85 90 95

Leu Pro His Val Ser Ala Asn Ala Ser Tyr Gln Arg Gln Pro Pro Ser

Ile Ser Ser Thr Arg Glu Thr Gln Giy Trp Ser Val Gln Val Gly Gln

Thr	Leu 130	Phe	Asp	Ala	Ala	Lys 135	Phe	Ala	Gln	Tyr	Arg 140	Gln	Ser	Arg	Phe
Asp 145	Thr	Gln	Ala	Ala	Glu 150	Gln	Arg	Phe	Asp	Ala 155	Ala	Arg	Glu	Glu	Leu 160
Leu	Leu	Lys	Val	Ala 165	Glu	Ser	Tyr	Phe	Asn 170	Val	Leu	Leu	Ser	Arg 175	Asp
Thr	Val	Ala	Ala 180	His	Ala	Ala	Glu	Lys 185	Glu	Ala	Tyr	Ala	Gln 190	Gln	Val
Arg	Gln	Ala 195	Gln	Ala	Leu	Phe	Asn 200	Г'nз	Gly	Ala	Ala	Thr 205	Ala	Leu	Asp
Ile	His 210	Glu	Ala	Lys	Ala	Gly 215	Tyr	Asp	Asn	Ala	Leu 220	Ala	Gln	Glu	Ile
Ala 225	Val	Leu	Ala	Glu	Lys 230	Gln	Thr	Tyr	Glu	Asn 235	Gln	Leu	Asn	Asp	Tyr 240
Tnr	Asp	Leu	Asp	Ser 245	rvs	Gln	Ile	Glu	Ala 250	lle	Asp	Thr	Ala	Asn 255	Leu
Leu	Äla	Arg	Tyr 260	Leu	Pro	Lys	Leu	Glu 265	Arg	Târ	Ser	Leu	Asp 270	Glu	Trp
Gln	Arg	lle 275	Ala	Leu	Ser	Asn	Asn 260	His	Glu	Tyr	Arg	Met 285	Gln	Gln	Leu
Ala	190 290	Gln	Ser	Ser	GT?	Gln 295	Ala	Leu	Arg	Ala	Ala 300	Cln	Asn	Ser	Arg
Тут 305	Pro	Thr	Val	Ser	Ala 310	Ris	Val	Gly	Tyr	Gln 315	Asn	Asn	Leu	Tyr	Tnr 320
Ser	Ser	Ala	Gln	Asn 325	Asn	Aep	Tyr	His	Tyr 330	Arg	Gly	Lys	Gly	Met 335	Ser
Val	Gly	Val	Gln 340	Leu	Asn	Leu	Pro	Leu 345		Thr	Gly	Gly	Glu 350	Leu	Ser
Gly	Lys	Ile 355		Glu	Ala	Glu	Ala 360		Tyr	Gly	Ala	Ala 365	Glu	Ala	Gln
Leu	Thr 370		Thr	Glu	Arg	H18		L', E	Leu	Ala	Val 380		Gln	Ala	Tyr
Thr 385		Ser	Gly	Ala	Ala 390		Tyr	Gln	. Ile	Met 395		Gln	Glu	Arg	Val 400
Leu	Glu	Ser	Ser	Arg 405		Lys	Leu	Lys	Ser 413		. Gln	Thr	Gly	Gln 415	
Tyr	Gly	Ile	Arg 420		Arg	Leu	Glu	Val 425		e Arg	Ala	. Arg	Gln 430		Val
Ala	Gln	Ala	Glu	Gln	Lys	. Leu	Ala	Glr	. Ala	Arg	Tyr	. TAs	; P'ne	: Met	Leu

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Ala Tyr Leu Arg Leu Val Lys Glu Ser Gly Leu Gly Leu Glu Thr Val
450 455 460
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Phe Ala Glu 465

<210> 31

<211> 696

<212> DNA

<213> Neisseria meningitidis

<220>

<221> CDS

<222> (1)..(693)

<400> 31

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Met Lys Gln Ser Ala Arg Ile Lys Asn Met Asp Gln Thr Leu Lys Asn
1 10 15

aca tig ggc att igc gcg cii ila gcc til igt til ggc gcg gcc atc 96
Thr Leu Gly Ile Cys Ala Leu Leu Ala Phe Cys Phe Gly Ala Ala Ile
25

gca toa ggt tat cae tig gaa tat gaa tae gge tae egi tat tet gee 144 Ala Ser Gly Tyr Ris Leu Glu Tyr Glu Tyr Gly Tyr Arg Tyr Ser Ala 35 40 45

tto dog dge gtt tot toa gtt gtt tia dtg att tad gtd gge ada add 240 Pne Pro Arg Val Ser Ser Val Val Leu Leu Ile Tyr Val Gly Thr Thr

gcc cta tat ttg ccg gtc ggc tgg ctg tat ggt gcg ccg tct tat cag 268
Ala Leu Tyr Leu Pro Val Gly Trp Leu Tyr Gly Ala Pro Scr Tyr Gln
85 90

ata gto ggt tog ata ttg gaa ago aat oot goo gag gog ogt gaa ttt 336 Ile Val Gly Ser Ile Leu Glu Ser Asn Pro Ala Glu Ala Arg Glu Phe 100 105

gto ggo aat cit dee ggg teg cit tat tit gtg dag gda tia tit tito 384 Val Gly Asn Leu Pro Gly Ser Leu Tyr Pne Val Gln Ala Leu Phe Phe 115 120 125

att ttt ggc ttg aca gtt tgg aga tat tgt gta tcg ggg ggg gta ttt 432 Ile Phe Gly Leu Thr Val Trp Arg Tyr Cys Val Ser Gly Gly Val Phe 130 135 140

gct gac gta aaa aac tat aaa cgc cgc agc aaa ata tgg ctg act ata 480 Ala Asp Val Lys Asn Tyr Lys Arg Arg Ser Lys Ile Trp Leu Thr Ile 145 150 160

The state of the s

									gcc Ala 175		528
									att Ile	ttc Phe	576
									cgc Arg		624
 _			-	_		_	•	_	gca Ala		672
tca Ser			_	taa							696

<210> 32

<211> 231

<212> PRT

<213> Neisseria meningitidis

 4400> 32

 Met Lys Gin Ser Ala Arg Ile Lys Asn Met Asp Gin Thr Leu Lys Asn 10
 10
 15
 Asn 15

 Thr Leu Gly Ile Cys Ala Leu Leu Pla Pla Pne Cys Phe Gly Ala Ala Ile 20
 20
 Ala Leu Leu Pro Gly Tyr Gly Tyr Arg Tyr Ser Ala 45

 Ala Ser Gly Tyr His Leu Glu Tyr Glu Tyr Gly Tyr Arg Tyr Ser Ala 35
 45
 Arg Gly Tyr Ser Ala 45

 Val Gly Ala Leu Ala Ser Val Val Pne Leu Leu Leu Leu Ala Arg Gly 50
 60
 60

 Phe Pro Arg Val Ser Ser Val Val Leu Leu lle Tyr Val Gly Thr Thr 75
 80

 Ala Leu Tyr Leu Pro Val Gly Trp Leu Tyr Gly Ala Pro Ser Tyr Gln 65
 90
 90

 Ile Val Gly Ser Ile Leu Glu Ser Asn Pro Ala Glu Ala Arg Glu Phe 100
 90
 95

 Ile Val Gly Asn Leu Pro Gly Ser Leu Tyr Phe Val Gln Ala Leu Phe Phe 125
 125

 Ile Phe Gly Leu Thr Val Trp Arg Tyr Cys Val Ser Gly Gly Val Phe 130
 135

 Ala Asp Val Lys Asn Tyr Lys Arg Arg Ser Lys Ile Trp Leu Thr Ile 145
 150

 Leu Leu Thr Leu Ile Leu Ser Cys Ala Val Met Asp Lys Ile Ala Ser 175

Asp Lys Asp Leu Arg Glu Pro Asp Ala Gly Leu Leu Leu Asn Ile Phe

Asp Leu Tyr Tyr Asp Leu Ala Ser Ala Pro Ala Pro Ile Cys Arg Gln
195 200 205

Ala Arg Pro His Phe Gly Ser Ser Lys Lys Ser Val Asn Met Ala Tyr 210 215 220

Pro Ser Cys Cys Ala Gln Val 225 230

<210> 33

<211> 909

<212> DNA

<213> Neisseria meningitidis

<220>

<221> CDS

<222> (1)..(906)

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140

 	-		_		_		~	tcc Ser	480
								ttg Leu 175	528
								ggt Gly	576
								gcg Ala	624
								gat Asp	672
								ttt Phe	720
								pro 255	768
								gaa Glu	815
								ocg Pro	864
						aaa Lys		tga	909

<210> 34

<211> 302

<212> PRT

<213> Neisseria meningitidis

<400> 34

Met Asr Val Tyr Sly Pne Pro Leu Pro Asp Thr Pro Phe Leu Ser Arg

Thr Lys Gly Leu Leu Ile Ash Gly Tyr Ris Phe Thr Ala His Ala Thr $20 \\ 25 \\ 30$

Ash Leu Ser Leu Pro Gin Thr Leu Gly Leu Pro Gly Glu Pro Ash Ash 35

Asn Ile Val Ser Leu Ala Lys Gin Ala Sly Phe Arg Thr Ala Trp Leu 50 55 60

Ser Asn Gln Gly Met Leu Gly His Phe Ala Asn Glu Ile Ser Thr Tyr

65					70					75					80
Ala	Leu	Arg	Ser	Asp 85	Tyr	Pro	Trp	Phe	Thr 90	Gln	Arg	Gly	Asp	Tyr 95	Gly
Lys	Ser	Ala	100 Gly	Leu	Ser	Asp	Arg	Leu 105	Leu	Leu	Pro	Ala	Phe 110	Lys	Arg
Val	Leu	Ile 115	Gly	Asn	Ala	Gly	Thr 120	Lys	Pro	Arg	Leu	Ile 125	Val	Met	His
Leu	Met 130	Gly	Ser	His	Ser	Asp 135	Phe	Сув	Thr	Arg	Leu 140	Asp	Lys	Asp	Ala
Arg 145	Arg	Phe	Gln	Tyr	Gln 150	Thr	Glu	Lys	Ile	Ser 155	Cys	Tyr	Val	Ser	Thr 160
Ile	Ala	Gln	Thr	Asp 165	Lys	Phe	Leu	Glu	Asp 170	Thr	Val	Lys	Ile	Leu 175	Asn
Glu	Asn	Lys	Glu 180	Ser	Trp	Ser	Leu	Val 185	Tyr	Phe	Ser	Asp	His 190	Gly	Leu
Met	His	Val 195	Gly	Lys	Gly	Gly	Glu 200	Arg	Thr	Leu	Thr	His 205	Gly	Ala	Trp
Lys	Arg 210		Ser	Tyr	Gly	Val Ils	Pro	Leu	Val	Lys	Ile 220	Ser	Ser	Asp	Asp
Thr 225		Arg	Glu	Met	Ile 230	Lys	Val	Arg	Arg	Ser 235		Phe	Asr.	Phe	Leu 240
Arg	Gly	Phe	Gly	Ser 245	Trp	Tar	G]?	Ile	Glu 250	Thr	Asp	Glu	Leu	Pro 255	Asp
Asp	Gly	Tyr	260		Trp	Gl;	Asn	Wal 265		e Asp	: Val	Gln	270	Glu	Gly
Asr	n Ast	Leu	a Ala	Phe	ile	Asp	Gly	Leu	. Pro	Asp	qaA o	Pro	: Ala	Pro	Trp

Tyr Ala Gly Lys Gly Lys Ser Thr Lys Asn Thr Ser Lys Lys 290 295 300

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<210> 35
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<211> 864

<212> DNA

<213> Neisseria meningitidis

<220>

<221> CDS

<222> (1)..(861)

t t

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Arg Ala Ala Ser Lys Ala Ala Leu Asn Val Tyr Glu Ala Ile Met Arg

250

245

gat ggc act tca ggc ggc ggt ggt gga cag tat gca aac ccg tgc cga Asp Gly Thr Ser Gly Gly Gly Gly Gln Tyr Ala Asn Pro Cys Arg 260 265 270

gct gta cga gca tct gaa cta tca tgc ctt cga gca aaa act gga taa 864 Ala Val Arg Ala Ser Glu Leu Ser Cys Leu Arg Ala Lys Thr Gly 275 280 285

<210> 36

<211> 287

<212> PRT

<213> Neisseria meningitidis

Glu Ser Asn Pro Leu Ala Val Ala Gly Cys Val Asn Ala Tyr Phe Ala 20 25 30

Arg Leu Ala Thr Gln Ser Gly Phe Lys Ala Ile Tyr Leu Ser Gly Gly 35 40

Gly Val Ala Ala Cys Ser Cys Gly Ile Pro Asp Leu Gly Ile Thr Thr 50 60

Met Glu Asp Val Leu Ile Asp Ala Arg Arg Ile Thr Asp Asn Val Asp 65 70 75 80

Thr Pro Leu Leu Val Asp Ile Asp Val Gly Trp Gly Gly Ala Phe Asn 85 95

Die Ala Arg Thr Die Arg Ash Phe Glu Arg Ala Gly Val Ala Ala Val 105 110

His Ile Glu Asp Gln Val Ala Gln Lys Arg Cys Gly His Arg Pro Asn 115 120 125

Lys Ala Tie Val Ser Lys Asp Glu Met Val Asp Arg Tie Lys Ala Ala 130 135

Val Asp Ala Arg Val Asp Glu Asn Yne Val IIe Met Ala Arg Thr Asp 145 150 156

Ala Leu Ala Val Glu Gly Leu Asp Ala Ala Ile Glu Arg Ala Gln Ala 165 170 175

Cys Val Glu Ala Gly Ala Asp Met Ile Pne Pro Glu Ala Met Thr Asp 180 185 190

Leu Asn Met Tyr Arg Gln Phe Ala Asp Ala Val Lys Val Pro Val Leu 195 200 205

Ala Asr Ile Thr Glu Phe Gly Ser Thr Pro Leu Tyr Thr Gln Ser Glu 210 215 220

Leu Ala Glu Asn Gly Val Ser Leu Val Leu Tyr Pro Leu Ser Ser Phe 225 230 235 240

Arg Ala Ala Ser Lys Ala Ala Leu Asn Val Tyr Glu Ala Ile Met Arg 245 250 255

Asp Gly Thr Ser Gly Gly Gly Gly Gln Tyr Ala Asn Pro Cys Arg 260 265 270

Ala Val Arg Ala Ser Glu Leu Ser Cys Leu Arg Ala Lys Thr Gly
275 280 285

<210> 37

<211> 921

<212> DNA

<213> Neisseria meningitidis

<220>

<221> CDS

<222> (1)..(918)

<400> 37

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Met Pro Ser Ser Lys Asn Trp Ile Asn Cys Phe Lys Asn Asp Leu Pro

CIT toa gao tgo cit toa ada aat cop dat ogg tog tot gaa aac cop 96 Leu Ser Asp Cys Leu Ser Tor Asn Pro His Arg Ser Ser Glu Asn Pro

Base occ ata asa asa cas agg aga ast ato atg act gas act act cas 144 Lys Pro Ile Lys Thr Gin Arg Arg Ash Thr Met Thr Giu Thr Thr Gin 35

acc deg acc etc asa ect asa asa tec ett ege ett tet ege ett ege 192
Thr Pro Thr beu Lys Pro bys byc Ser hal Ala beu Ser Gly Val Ala
50 55

god ggt aat acc got tig tgt acc gtt ggc ogt acc ggc aac gat tig 240 Ala Gly Asn Thr Ala Leu Cys Thr Val Gly Arg Thr Gly Asn Asp Leu 65 70 75 80

ago tat ogo ggt tao gao att otg gat ttg gca caa aaa tgt gag ttt 288 Ser Tyr Arg Gly Tyr Asp lle Leu Asp Leu Ala Gln Lys Cys Glu Phe

gaa gaa git goo dad dig dig ati dad ggo dat tia doo aad ada tio 336 Glu Glu Val Ala His Leu Leu Ile His Gly His Leu Pro Asn Lys Phe

gag ctg gcc gct tal aaa gcc aag ctl aaa toc atg cgc ggc ctg cct 384 Glu Leu Ala Ala Tyr Lys Ala Lys Leu Lys Ser Met Arg Gly Leu Pro 115 120 125

atc cgt gtg att aaa gtt ttg gaa agc ctg cct gca cat acc cat ccg 432
 Ile Arg Val Ile Lys Val Leu Glu Ser Leu Pro Ala His Thr His Pro 130
 140

atg gac gtg atg cgt acc ggc gta too atg ctg ggc tgt gtt cat cct 480 Met Asp Val Met Arg Thr Gly Val Ser Met Leu Gly Cys Val His Pro 150 155 160

														gac Asp 175		528
														tat Tyr		576
cac His	aac Asn	ggc Gly 195	aaa Lys	cgc Arg	att Ile	gaa Glu	gtt Val 200	gaa Glu	agc Ser	gaa Glu	gaa Glu	gag Glu 205	acc Thr	atc Ile	gjà âãc	624
														tca Ser		672
		_	_		-		_		_		_	-		gag Glu		720
														tct Ser 255		768
			_				_				-			ccg Pro		816
														acc Thr		864
														gsa Ala		912
	tog Ser	tga														921

<210> 38

<211> 306

<212> PRT

<213> Neisseria meningitidis

<400> 38

Met Pro Ser Ser Lys Asn Trp Ile Asn Cys Phe Lys Asn Asp Leu Pro 1 5 10

Leu Ser Asp Cys Leu Ser Thr Asn Pro His Arg Ser Ser Glu Asn Pro 20 25 30

Lys Pro Ile Lys Thr Gln Arg Arg Asn Thr Met Thr Glu Thr Thr Gln 35 40

Thr Pro Thr Leu Lys Pro Lys Lys Ser Val Ala Leu Ser Gly Val Ala 50 60

Ala Gly Asn Thr Ala Leu Cys Thr Val Gly Arg Thr Gly Asn Asp Leu 65 70 75 80

Ser Tyr Arg Gly Tyr Asp Ile Leu Asp Leu Ala Gln Lys Cys Glu Phe 85 90 95

Glu Glu Val Ala His Leu Leu Ile His Gly His Leu Pro Asn Lys Phe 100 105 110

Glu Leu Ala Ala Tyr Lys Ala Lys Leu Lys Ser Met Arg Gly Leu Pro 115 120 125

Ile Arg Val Ile Lys Val Leu Glu Ser Leu Pro Ala His Thr His Pro 130 135 140

Met Asp Val Met Arg Thr Gly Val Ser Met Leu Gly Cys Val His Pro 145 . 150 . 155 . 160

Glu Arg Glu Gly His Pro Glu Ser Glu Ala Arg Asp Ile Ala Asp Lys 165 170 175

Leu Ile Ala Ser Leu Gly Ser Ile Leu Leu Tyr Trp Tyr Gln Tyr Ser 180 185 190

His Asn Gly Lys Arg Ile Glu Val Glu Ser Glu Glu Glu Thr Ile Gly
195 200 205

Gly His Phe Leu His Leu Leu His Gly Lys Arg Pro Ser Glu Ser His 210 215 220

Ile Lys Ala Met His Val Ser Leu Ile Leu Tyr Ala Glu His Glu Phe 225 230 235

Asn Ala Ser Thr Phe Thr Ala Arg Val Ile Ala Gly Thr Gly Ser Asp 245 250 255

Met Tyr Ser Ser Ile Thr Gly Ala Ile Gly Ala Leu Lys Gly Pro Lys 260 265 270

His Gly Gly Ala Asn Glu Gly Leu Thr Ile Phe Lys Asn Ala Thr Ala 275 280 285

Met Pro Thr Lys Pro Lys Pro Thr Ser Ala Asn Ala Ser Ala Ala Lys 290 295 300

Lys Ser

<210> 39

<211> 945

<212> DNA

<213> Neisseria meningitidis

<220>

<221> CDS

<222> (1)..(942)

atg cac cta tgt gga aag tat tat gga gta aat atg aag ctg cgt gat Met His Leu Cys Gly Lys Tyr Tyr Gly Val Asn Met Lys Leu Arg Asp tta ctg atg gga ata ttc ttg gca gtt tct gcg gcc ctt ctg aat gca Leu Leu Met Gly Ile Phe Leu Ala Val Ser Ala Ala Leu Leu Asn Ala acc atc ggc ata ttc agc aag ata ttg atg gag cag ggc ttg tct gtt Thr Ile Gly Ile Phe Ser Lys Ile Leu Met Glu Gln Gly Leu Ser Val cag cat att gca tit ttg aaa act tig aca ggt ttc gtg tit atc agc 192 Gln His Ile Ala Phe Leu Lys Thr Leu Thr Gly Phe Val Phe Ile Ser att ttg ctt tgc cgt acc ggt ttt acc aga cag att gcg gat att tca Ile Leu Leu Cys Arg Thr Gly Phe Thr Arg Gln Ile Ala Asp Ile Ser aga aag aaa gag gca att ttg ccg ttg ctg tta aaa gta gca att tgt 288 Arg Lys Lys Glu Ala Ile Leu Pro Leu Leu Lys Val Ala Ile Cys gct ttt ttc gga att tat acg ttg ttt ttc ttt gaa acc aca gct tat Ala Phe Phe Gly Ile Tyr Thr Leu Phe Phe Phe Glu Thr Thr Ala Tyr 100 caa tat ggc aat gct gcg aat gta gta gtt gta tta atg gca tcg gct Gln Tyr Gly Asn Ala Ala Asn Val Val Val Leu Met Ala Ser Ala gcc gta tct gcc ttg ata ttg gac agc ata ctg tta gat gaa cgt att Ala Val Ser Ala Leu Ile Leu Asp Ser Ile Leu Leu Asp Glu Arg Ile 130 135 140 tgc att tet tea gte gte ggt gtg ggt ttg gea gta ttg ggg ate gea Cys Ile Ser Ser Val Val Gly Val Gly Leu Ala Val Leu Gly Ile Ala atg att tot tgg act gga gaa gga agt tta ggg ttg att ctg aat gec 528 Met Ile Ser Trp Thr Gly Glu Gly Ser Leu Gly Leu Ile Leu Asn Ala 170 gea etg geg gge teg gge tae ggt tgt ttt tee gtt ttg att aag aaa Ala Leu Ala Gly Ser Gly Tyr Gly Cys Phe Ser Val Leu Ile Lys Lys ttc ggc cta aac ggc ggt att tat ttg aca cgg ata ttg atg ttt ttt Phe Gly Leu Asn Gly Gly Ile Tyr Leu Thr Arg Ile Leu Met Phe Phe 195 200 gga agt att ttt ttg ttt atc cct tca ttg gaa ggt att gag gat ata Gly Ser Ile Phe Leu Phe Ile Pro Ser Leu Glu Gly Ile Glu Asp Ile 215 cat tgg caa tgg tot ttl att ccg cca ctc ttg gca ttg tot tta ttg His Trp Gln Trp Ser Phe Ile Pro Pro Leu Leu Ala Leu Ser Leu Leu 235

ddg adg att tta gga ttt tat tgt ada act aaa gda ttg gat tat ttg Pro Thr Ile Leu Gly Phe Tyr Cys Thr Thr Lys Ala Leu Asp Tyr Leu 245 agt gct gcg aag gta cag gta act gaa ttg gcc gag cca ttg ttt gct 816 Ser Ala Ala Lys Val Gln Val Thr Glu Leu Ala Glu Pro Leu Phe Ala 265 gcc gta ctg gct tgg ttg ttt ttg aat gaa ata ccg gaa gga cgc ttc Ala Val Leu Ala Trp Leu Phe Leu Asn Glu Ile Pro Glu Gly Arg Phe 280 ttt gro ggo goo att otg att att goo ggt att gtg tot atc aat ggg Phe Val Gly Ala Ile Leu Ile Ile Ala Gly Ile Val Ser Ile Asn Gly 290 295 945 ctg tat cga cca ttg ttg aag cga att gaa taa Leu Tyr Arg Pro Leu Leu Lys Arg Ile Glu 305

<210> 40

<211> 314

<212> PRT

<213> Neisseria meningitidis

<400> 40

Met His Leu Cys Gly Lys Tyr Tyr Gly Val Asn Met Lys Leu Arg Asp 1 10 15

Leu Leu Met Gly Ile Phe Leu Ala Val Ser Ala Ala Leu Leu As
n Ala 20 25 30

Thr Ile Gly Ile Phe Ser Lys Ile Leu Met Glu Gln Gly Leu Ser Val
35 40

Gln His Ile Ala Phe Leu Lys Thr Leu Thr Gly Phe Val Phe Ile Ser 50 60

Ile Leu Leu Cys Arg Thr Gly Phe Thr Arg Gln Ile Ala Asp Ile Ser 65 70 75 80

Arg Lys Lys Glu Ala Ile Leu Pro Leu Leu Leu Lys Val Ala Ile Cys 85 90 95

Ala Phe Phe Gly Ile Tyr Thr Leu Phe Phe Phe Glu Thr Thr Ala Tyr 100 105 110

Gln Tyr Gly Asn Ala Ala Asn Val Val Val Leu Met Ala Ser Ala 115 120 125

Ala Val Ser Ala Leu Ile Leu Asp Ser Ile Leu Leu Asp Glu Arg Ile 130 140

Cys Ile Ser Ser Val Val Gly Val Gly Leu Ala Val Leu Gly Ile Ala 145 150 155 160

Met Ile Ser Trp Thr Gly Glu Gly Ser Leu Gly Leu Ile Leu Asn Ala 165 170 175 Ala Leu Ala Gly Ser Gly Tyr Gly Cys Phe Ser Val Leu Ile Lys Lys 180 185 190

Phe Gly Leu Asn Gly Gly Ile Tyr Leu Thr Arg Ile Leu Met Phe Phe 195 200 205

Gly Ser Ile Phe Leu Phe Ile Pro Ser Leu Glu Gly Ile Glu Asp Ile 210 215 220

His Trp Gln Trp Ser Phe Ile Pro Pro Leu Leu Ala Leu Ser Leu Leu 225 230 235 240

Pro Thr Ile Leu Gly Phe Tyr Cys Thr Thr Lys Ala Leu Asp Tyr Leu 245 250 255

Ser Ala Ala Lys Val Gln Val Thr Glu Leu Ala Glu Pro Leu Phe Ala 260 . 265 270

Ala Val Leu Ala Trp Leu Phe Leu Asn Glu Ile Pro Glu Gly Arg Phe 275 280 285

Phe Val Gly Ala Ile Leu Ile Ile Ala Gly fle Val Ser Ile Asn Gly 290 295 300

Leu Tyr Arg Pro Leu Leu Lys Arg Ile Glu 305

<210> 41

int in the second

<211> 2610

<212> DNA

<213> Neisseria meningitidis

<220>

<221> CDS

<222> (1)..(2607)

<400> 41

atg gct gcc aac caa cgt tac cgc aaa ccg ctg ccc ggt acg gat ttg 48
Met Ala Ala Asn Gln Arg Tyr Arg Lys Pro Leu Pro Gly Thr Asp Leu
1 5 10 15

gaa tac tac gac gcg cgt gcg gcg tgt gag gac atc aag ccc ggc tct 96 Glu Tyr Tyr Asp Ala Arg Ala Ala Cys Glu Asp Ile Lys Pro Gly Ser 20 25 30

tac gac aag ctg cct tac acg agc cgc att ttg gcg gag aat ttg gtc 144
Tyr Asp Lys Leu Pro Tyr Thr Ser Arg Ile Leu Ala Glu Asn Leu Val
35 40

aac cgc gcg gac aaa gtc gat ttg ccg acg ctg caa agc tgg ctg ggt 192
Asn Arg Ala Asp Lys Val Asp Leu Pro Thr Leu Gln Ser Trp Leu Gly
50 55 60

cag ctg att gag gga aaa cag gaa atc gac ttt cct tgg tat ccg gcg 240 Gln Leu Ile Glu Gly Lys Gln Glu Ile Asp Phe Pro Trp Tyr Pro Ala 65 70 75 80

cgg gtg gtg tgc cac gat att ctg ggg cag acc gcg ttg gtg gat ttg 288

AT A STATE OF THE
Arg	Val	Val	Cys	His 85	Asp	Ile	Leu	Gly	Gln 90	Thr	Ala	Leu	Val	Asp 95	Leu	
gca Ala	ggt Gly	ctg Leu	cgc Arg 100	gat Asp	gcg Ala	att Ile	gcc Ala	gaa Glu 105	aaa Lys	ggc Gly	ggc	gat Asp	cct Pro 110	gcc Ala	aaa Lys	336
gtg Val	aat Asn	ccg Pro 115	gtg Val	gtt Val	gca Ala	aaa Lys	ccc Pro 120	agc Ser	ttc Phe	atc Ile	gtc Val	gac Asp 125	cac His	tct Ser	ctg Leu	384
gcc Ala	gtt Val 130	gaa Glu	tgc Cys	ggc Gly	ggc Gly	tac Tyr 135	gac Asp	ccc Pro	gat Asp	gcc Ala	ttc Phe 140	cgc Arg	aaa Lys	aac Asn	cgc Arg	432
caa Gln 145	atc Ile	gaa Glu	gac Asp	aga Arg	cgt Arg 150	aac Asn	gaa Glu	gac Asp	cgt Arg	ttc Phe 155	cac His	ttc Phe	atc Ile	aac Asn	tgg Trp 160	480
aca Thr	aaa Lys	acc Thr	gca Ala	ttt Phe 165	gaa Glu	aat Asn	gtg Val	gac Asp	gtg Val 170	att Ile	ccg Pro	gcg Ala	ggc Gly	aac Asn 175	ggc	528
atc Ile	atg Met	cac His	caa Gln 180	atc Ile	aat Asn	cta Leu	gaa Glu	aaa Lys 185	atg Met	tcg Ser	ccc Pro	gtc Val	gtc Val 190	caa Gln	gtc Val	576
aaa Lys	aac Asn	ggc Gly 195	gtg Val	gcg Ala	ttc Phe	ccc Pro	gat Asp 200	acc Thr	tgc Cys	gtc Val	ggc	acg Thr 205	gat Asp	tcg Ser	cac His	624
acg Thr	ccg Pro 210	Cac His	gtc Val	gat Asp	gcg Ala	ctg Leu 215	gly	gtg Val	att Ile	tcc Ser	gtg Val 220	ggc Gly	gtg Val	ggc Gly	gga Gly	672
ttg Leu 225	gaa Glu	gcg Ala	gaa Glu	acc Thr	gtg Val 230	atg Met	ctg Leu	ggt Gly	cgc Arg	gcg Ala 235	Ser	atg Met	atg Met	cgc Arg	ctg Leu 240	720
ccc Pro	gat Asp	att Ile	gtc Val	ggc Gly 245	gtt Val	gag Glu	ctg Leu	aac Asn	ggc Gly 250	Lys	cgg Arg	cag Gln	gcg Ala	ggc Gly 255	Ile	768
acg Thr	gcg	acg Thr	gat Asp 260	Ile	gtg Val	ttg Leu	gca Ala	ctg Leu 265	Thr	gaç Glu	ttt Phe	. ctg : Leu	ege Arg 270	Lys	gaa Glu	816
cgc Arg	gtg Val	gto Val 275	Gly	gcg Ala	ttt Phe	gtc Val	gaa Glu 280	Phe	tto Phe	: Gly	gag Glu	ggc Gly 285	Ala	aga Arg	agc Ser	864
ctg Leu	tct Ser 290	Ile	: Gly	gac Asp	cgc Arg	gcg Ala 295	Thr	att	tcc Ser	aac Asr	ate 1 Met 300	Thr	Pro	gag Glu	ttc Phe	912
ggc Gly 305	Ala	act Thr	gco Ala	gcg Ala	atg Met 310	. Phe	gct Ala	att Ile	gat Asp	gag Glu 319	ı Glı	a acc	: att	gat Asp	tat Tyr 320	960
ttg	aaa	cto	g acc	ggs	cgc	ga c	gad	ges	cas	ggt	g aaa	a tts	gte	gaa	acc	1008

Leu	Lys	Leu	Thr	Gly 325	Arg	Asp	Ąsp	Ala	Gln 330	Val	Lys	Leu	Val	Glu 335	Thr	
												aaa Lys				1056
												acg Thr 365				1104
gca Ala	ggc Gly 370	ccg Pro	agc Ser	aac Asn	ccg Pro	cac His 375	gcg Ala	cgt Arg	ttt Phe	gcg Ala	acc Thr 380	gcc Ala	gat Asp	ttg Leu	gcc Ala	1152
agc Ser 385	aaa Lys	ggc	ttg Leu	gct Al·a	aaa Lys 390	cct Pro	tac Tyr	gaa Glu	gag Glu	cct Pro 395	tca Ser	gac Asp	ggc	caa Gln	atg Met 400	1200
												tgc Cys				1248
												gcg Ala				1296
												acc Thr 445				1344
												gca Ala				1392
												ttc Phe				1440
												atc Ile				1488
												tca Ser			ege Arg	1536
								Tyr				gct Ala 525	Phe		gct Ala	1584
		Pro					Tyr								ttc Phe	1632
	Ile					Leu					Gly				ege Arg 560	1680
ctg	aaa	gac	att	tgg	cct	gca	gat	. gaa	gaa	ato	gat	gco	gto	gtt	gcc	1728

Leu	Lys	qaA	Ile	Trp 565	Pro	Ala	Asp	Glu	Glu 570	Ile	qzA	Ala	Val	Val 575	Ala	
			aaa Lys 580													1776
			aca Thr													1824
			acc Thr			_	_									1872
			cgc Arg													1920
			acc Thr		_											1968
			gca Ala 660													2016
			tct Ser													2064
			ttc Phe													2112
			agc Ser		_					-	-	-				2160
			atg Met													2208
			ctc Leu 740													2256
			tgg Trp													2304
		Ala										Asn			Gly	2352
	Gly		ttg Leu								Thr					2400
ctg	caa	ctg	gac	ggt	acg	gaa	acc	tac	gac	gtg	gtc	ggc	gaa	cãc	aca	2448

APPENDING THE PROPERTY.

<210> 42

<211> 869

<212> PRT

<213> Neisseria meningitidis

Glu Tyr Tyr Asp Ala Arg Ala Ala Cys Glu Asp Ile Lys Pro Gly Ser 20 25 30

Tyr Asp Lys Leu Pro Tyr Thr Ser Arg Ile Leu Ala Glu Asn Leu Val 35 40 45

Asn Arg Ala Asp Lys Val Asp Leu Pro Thr Leu Gln Ser Trp Leu Gly 50 60

Gln Leu Ile Glu Gly Lys Gln Glu Ile Asp Phe Pro Trp Tyr Pro Ala 65 70 75 80

Arg Val Val Cys His Asp Ile Leu Gly Gln Thr Ala Leu Val Asp Leu 85 90 95

Ala Gly Leu Arg Asp Ala Ile Ala Glu Lys Gly Gly Asp Pro Ala Lys 100 \$105\$

Val Asn Pro Val Val Ala Lys Pro Ser Phe Ile Val Asp His Ser Leu 115 120 125

Ala Val Glu Cys Gly Gly Tyr Asp Pro Asp Ala Phe Arg Lys Asm Arg 130 135

· Gin Ile Glu Asp Arg Arg Asn Glu Asp Arg Phe His Phe Ile Asn Trp
145 150 150 160

Thr Lys Thr Ala Phe Glu Asn Val Asp Val Ile Pro Ala Gly Asn Gly 165 170 175

Ile Met His Gln Ile Asn Leu Glu Lys Met Ser Pro Val Val Gln Val

185

500 . 505 510

Asn Phe Asp Gly Arg Val His Pro Tyr Ala Lys Gln Ala Phe Leu Ala Ser Pro Pro Leu Val Val Ala Tyr Ala Leu Ala Gly Ser Ile Arg Phe Asp Ile Glu Asn Asp Val Leu Gly Val Ala Asp Gly Lys Glu Ile Arg Leu Lys Asp Ile Trp Pro Ala Asp Glu Glu Ile Asp Ala Val Val Ala Glu Tyr Val Lys Pro Gln Gln Phe Arg Asp Val Tyr Val Pro Met Phe 580 585 Asp Thr Gly Thr Ala Gln Lys Ala Pro Ser Pro Leu Tyr Asp Trp Arg 600 Pro Met Ser Thr Tyr Ile Arg Arg Pro Pro Tyr Trp Glu Gly Ala Leu Ala Gly Glu Arg Thr Leu Arg Gly Met Arg Pro Leu Ala Ile Leu Pro 635 Asp Asn Ile Thr Thr Asp His Leu Ser Pro Ser Asn Ala Ile Leu Ala 645 Val Ser Ala Ala Gly Glu Tyr Leu Ala Lys Met Gly Leu Pro Glu Glu Asp Phe Asn Ser Tyr Ala Thr His Arg Gly Asp His Leu Thr Ala Gln 680 Arg Ala Thr Phe Ala Asn Pro Lys Leu Phe Asn Glu Met Val Lys Asn 695 Glu Asp Gly Ser Val Arg Gln Gly Ser Phe Ala Arg Val Glu Pro Glu Gly Glu Thr Met Arg Met Trp Glu Ala Ile Glu Thr Tyr Met Asn Arg Lys Gln Pro Leu Ile Ile Ile Ala Gly Ala Asp Tyr Gly Gln Gly Ser Ser Arg Asp Trp Ala Ala Lys Giy Val Arg Leu Ala Gly Val Glu Ala 755 760 Ile Val Ala Glu Gly Phe Glu Arg Ile His Arg Thr Asn Leu Ile Gly Met Gly Val Leu Pro Leu Gln Phe Lys Pro Asp Thr Asn Arg His Thr 785 795 Leu Gln Leu Asp Gly Thr Glu Thr Tyr Asp Val Val Gly Glu Arg Thr Pro Arg Cys Asp Leu Thr Leu Val Ile His Arg Lys Asn Gly Glu Thr 820 . 825 830

Val Glu Val Pro Val Thr Cys Arg Leu Asp Thr Ala Glu Glu Val Leu 835 840 845

Val Tyr Glu Ala Gly Gly Val Leu Gln Arg Phe Ala Gln Asp Phe Leu 850 860

Glu Gly Asn Ala Ala 865

<210> 43

<211> 1170

<212> DNA

<213> Neisseria meningitidis

<220>

<221> CDS

<222> (1)..(1167)

<400> 43

atg ccg caa att aaa att ccc gcc gtt tac tac cgt ggc ggt aca tca 48
Met Pro Gln Ile Lys Ile Pro Ala Val Tyr Tyr Arg Gly Gly Thr Ser
1 5 10 15

aaa ggc gtg ttt ttc aaa cgt tcc gac ctg ccc gag geg gcg cgg gaa 96 Lys Gly Val Phe Phe Lys Arg Ser Asp Leu Pro Glu Ala Ala Arg Glu 20 25 30

gac coe tae gge aag cag ata gac ggt ttg gge aac gee agt teg tee 192
Asp Pro Tyr Gly Lys Gln Ile Asp Gly Leu Gly Asn Ala Ser Ser Ser
50 60

acc agc aaa gcc gtg att ttg gac aag tcc gaa cgc acc gat cac gat
Thr Ser Lys Ala Val Ile Leu Asp Lys Ser Glu Arg Thr Asp His Asp
65 70 80

gtc gat tac ctt ttc ggg caa gtt tcc atc gac aaa cct ttt gtc gat 288 Val Asp Tyr Leu Phe Gly Gln Val Ser Ile Asp Lys Pro Phe Val Asp 85 90 95

tgg agt ggc aac tgc ggc aac ctc acc gcc gcc gtg ggc gca ttt gcc 336
Trp Ser Gly Asn Cys Gly Asn Leu Thr Ala Ala Val Gly Ala Phe Ala
100 105 110

atc gag caa ggc ttg gtc gat aaa tcc aaa atc cct tca gac ggc ccg 384 Ile Glu Gln Gly Leu Val Asp Lys Ser Lys Ile Pro Ser Asp Gly Pro 115 120 125

tgt acc gtc aaa atc tgg cag aaa aac atc ggc aaa acc att att gcc 432 Cys Thr Val Lys Ile Trp Gln Lys Asn Ile Gly Lys Thr Ile Ile Ala 130 135 . 140

cat gta cog atg caa aac ggc gca gtt ttg gaa aca ggc gat ttt gag 480

His Val Pr 145	o Met		sn Gly 50	Ala	Val :	Leu	Glu 155	Thr	Gly .	Asp	Phe	Glu 160	
ctc gac go Leu Asp Gl	gc gta .y Val	acg t Thr P	tc ccg he Pro	gca Ala	Ala	gaa Glu 170	gta Val	caa Gln	atc Ile	gaa Glu	ttt Phe 175	ctt Leu	528
gat cca go Asp Pro Al	cc gac la Asp 180	ggc g	aa ggo lu Gly	agt Ser	atg Met 185	ttc Phe	cca Pro	acc Thr	GIY	aat Asn 190	ttg Leu	gtc Val	576
gat gaa a Asp Glu I	ct gat le Asp 95	gtg c Val P	cg aat	ata 1 Ile 200	ggc Gly	cgt Arg	ttg Leu	aaa Lys	gcc Ala 205	acg Thr	ctc Leu	atc Ile	624
aac gcg gg Asn Ala G 210	gc att ly Ile	ccg a Pro T	icc gt Thr Va 21	l Phe	ctg Leu	aat Asn	gcc Ala	gcc Ala 220	gac Asp	ttg Leu	gly ggc	tac Tyr	672
acg ggc a Thr Gly L 225	aa gag ys Glu	Leu C	aa ga Sln As 230	c gac p Asp	atc Ile	aac Asn	aac Asn 235	gat Asp	gcc Ala	gca Ala	gct Ala	ttg Leu 240	720
gaa aaa t Glu Lys P	tc gag he Glu	aaa a Lys : 245	atc cg Ile Ar	c gct g Ala	tac Tyr	ggt Gly 250	gcg Ala	ctg Leu	aaa Lys	atg Met	ggt Gly 255	cta Leu	768
atc agc g Ile Ser A	ac gta sp Val	. Ser (gaa go Glu Al	t gcc a Ala	gcc Ala 265	cgc Arg	gcg Ala	cac His	acg Thr	ccg Pro 270	aaa Lys	gtc Val	816
gcc ttc g Ala Phe V	tc gcg al Ala	g ccc : Pro :	gee ge Ala Al	c gat a Asp 280	Tyr	acc Thr	gcc Ala	tcc Ser	agt Ser 285	ggc	aaa Lys	acc Thr	864
gtg aat g Val Asn A 290	gcc gcc Ala Ala	gac Asp	atc ga Ile As 29	p Let	g ctg 1 Leu	gta Val	cgc Arg	gcc Ala 300	ctg Leu	agc Ser	atg Met	ggc	912
aaa ttg d Lys Leu 1 305	cac cac	s Ala	atg at Met Me 310	g gg! at Gl:	acc y Thr	gcc Ala	tct Ser 315	. Val	gcc Ala	att	gcs Ala	acc Thr 320	960
gcc gcc (Ala Ala	gcc gt Ala Va	g ccc l Pro 325	ggt a Gly T	nr Le	g gto u Val	aac Asr 330	i Let	gco l Ala	gca Ala	Gly	g gcg / Ala 335	a Giy	1008
acg cgt Thr Arg	aaa ga Lys Gl 34	u Val	cgc t Arg P	tc gg he Gl	g cat y His 345	Pro	tco Sea	c ggo r Gly	aca Thr	ttg Lei 350	ı Ar	g gtc g Val	1056
ggt gca Gly Ala	gcc gc Ala Al 355	c gaa a Glu	tgt c Cys G	ag ga ln As 36	p Gly	a caa / Gl:	a tgg n Trj	g acq p Thi	g gcc Ala 369	a Th	c aar r Ly	a gcg s Ala	1104
gtt atg Val Met 370	agd dg Ser Ar	ge age g Ser	Ala A	gc gt rg Va 75	g atq 1 Me	g ato	g ga t Gl	a ggi u Gli 38	y TT]	g gt. p Va	c ag l Ar	g gtg g Val	1152
ccg gaa Pro Glu 385													1170

<210> 44

<211> 389

<212> PRT

<213> Neisseria meningitidis

Lys Gly Val Phe Phe Lys Arg Ser Asp Leu Pro Glu Ala Ala Arg Glu 20 25 30

Ala Gly Ser Ala Arg Asp Lys Ile Leu Leu Arg Val Leu Gly Ser Pro 35 40 45

Asp Pro Tyr Gly Lys Gln Ile Asp Gly Leu Gly Asn Ala Ser Ser Ser 50 55 60

Thr Ser Lys Ala Val Ile Leu Asp Lys Ser Glu Arg Thr Asp His Asp 65 70 75 80

Val Asp Tyr Leu Phe Gly Gln Val Ser Ile Asp Lys Pro Phe Val Asp 85 90 95

Trp Ser Gly Asn Cys Gly Asn Leu Thr Ala Ala Val Gly Ala Phe Ala 100 105 110

Ile Glu Gln Gly Leu Val Asp Lys Ser Lys Ile Pro Ser Asp Gly Pro 115 120 125

Cys Thr Val Lys Ile Trp Gln Lys Asn Ile Gly Lys Thr Ile Ile Ala 130 135 140

His Val Pro Met Gln Asn Gly Ala Val Leu Glu Thr Gly Asp Phe Glu 145 150 155 160

Leu Asp Gly Val Thr Phe Pro Ala Ala Glu Val Gln Ile Glu Phe Leu 165 170 175

Asp Pro Ala Asp Gly Glu Gly Ser Met Phe Pro Thr Gly Asn Leu Val

Asp Glu Ile Asp Val Pro Asn Ile Gly Arg Leu Lys Ala Thr Leu Ile 195 200 205

Asn Ala Gly Ile Pro Thr Val Phe Leu Asn Ala Ala Asp Leu Gly Tyr 210 225 220

Thr Gly Lys Glu Leu Gln Asp Asp Ile Asn Asn Asp Ala Ala Ala Leu 225 230 235 240

Glu Lys Phe Glu Lys Ile Arg Ala Tyr Gly Ala Leu Lys Met Gly Leu 245 250 255

Ile Ser Asp Val Ser Glu Ala Ala Ala Arg Ala His Thr Pro Lys Val 260 265 270 Ala Phe Val Ala Pro Ala Ala Asp Tyr Thr Ala Ser Ser Gly Lys Thr 275 280 285

Val Asn Ala Ala Asp Ile Asp Leu Leu Val Arg Ala Leu Ser Met Gly 290 295 300

Lys Leu His His Ala Met Met Gly Thr Ala Ser Val Ala Ile Ala Thr 305 310 315 320

Ala Ala Val Pro Gly Thr Leu Val Asn Leu Ala Ala Gly Ala Gly
325 330 335

Thr Arg Lys Glu Val Arg Phe Gly His Prc Ser Gly Thr Leu Arg Val 340 345

Gly Ala Ala Glu Cys Gln Asp Gly Gln Trp Thr Ala Thr Lys Ala 355 360 365

Val Met Ser Arg Ser Ala Arg Val Met Met Glu Gly Trp Val Arg Val 370 380

Pro Glu Asp Cys Phe

<210> 45

<211> 954

<212> DNA

<213> Neisseria meningitidis

<220>

<221> CDS

<222> (1)..(951)

<400> 45

atg ogc acg ccg ttt tgt tgg gca tac gcc aat gcc gcc cga ata tcg 48 Met Arg Thr Pro Phe Cys Trp Ala Tyr Ala Asn Ala Ala Arg Ile Ser 1 5 10 15

gca atg ctg ccg gcg tgt tgg gcg cag gcg atg ttg gcc gaa gta atc 96 Ala Met Leu Pro Ala Cys Trp Ala Gln Ala Met Leu Ala Glu Val Ile 20 25 30

ago tgo aac aag got tog tog ctg cog cag cot tog gog aga tog gog 144 Ser Cys Asn Lys Ala Ser Ser Leu Pro Gln Pro Ser Ala Arg Ser Ala 35

ttt aaa toa acc tgo tto atg ggt gat tot oog tat ttg gtt oag ata 192 Phe Lys Ser Thr Cys Phe Met Gly Asp Ser Pro Tyr Leu Val Gln Ile

gac ttg gtt ttt gcg ccg cag ggc ggt ggc ttc ttt caa gcc gat tat 240 Asp Leu Val Phe Ala Pro Gin Gly Gly Gly Phe Phe Gln Ala Asp Tyr 65 70 75 80

ttt gaa ttt gac ttt gct gcc gaa gcg cac ctg tgc cag cct gcc caa 288 Phe Glu Phe Asp Phe Ala Ala Glu Ala His Leu Cys Gln Pro Ala Gln 85 90

							gcc Ala			336
							cgg Arg 125			384
							agg Arg			432
							gtt Val			480
							ccc Pro			528
							ggt Gly			576
	 	_	-			_	cgc Arg 205		_	624
							ctg Leu			672
							cac His			720
							gcc Ala			768
							ata Ile			816
							cac His 285		ggt	864
									caa Gln	912
Asp							caa Gln			954

<210> 46

<211> 317

<212> PRT

<213> Neisseria meningitidis

<400> 46

μ1 (¹

Met Arg Thr Pro Phe Cys Trp Ala Tyr Ala Asn Ala Ala Arg Ile Ser
1 10 15

Ala Met Leu Pro Ala Cys Trp Ala Gln Ala Met Leu Ala Glu Val Ile 20 25 30

Ser Cys Asn Lys Ala Ser Ser Leu Pro Gln Pro Ser Ala Arg Ser Ala 35 40 45

Phe Lys Ser Thr Cys Phe Met Gly Asp Ser Pro Tyr Leu Val Gln Ile 50 55

Asp Leu Val Phe Ala Pro Gln Gly Gly Gly Phe Phe Gln Ala Asp Tyr 65 70 75 80

Phe Glu Phe Asp Phe Ala Ala Glu Ala His Leu Cys Gln Pro Ala Gln 85 90 95

Ile Gly Gly Asn Gly Ser Asp Phe Arg Ile Thr Ala Gly Gly Leu 100 105 110

Arg Ile Gly Gln Gln Asp Asn Arg Phe Ala Ala Gly Arg His Leu His

Giy Ser Cys Leu Asn Ser Val Gly Gln His Phe Gln Arg Leu Arg Gln 130 140

Gly Gln Arg Leu Ser Val Glu Ala Val Ala His Ala Val Ala Ile Ala 145 150 155

Leu Gln Arg Pro Arg Phe Pro Pne Gln Ile Gln Thr Pro Phe Phe Thr

Glu Ser Gly Ile Phe Arg Arg Arg Ash Lys Val Asp Gly Ile Gly Lys 180 185 190

Arg Tyr Arg Gly Asn Ala Asp The Gly Gln Fhe Leu Arg Thr Phe Ala 195 200 205

Asp Gly Glu Ile Ile Ala Phe Leu Gln His Ser Ala Leu Met Ala Ala 210 225 220

Glu Thr Gly Phe Gln Val Gly Ala Ser Arg Thr His His Phe Arg His 225 235 240

Ile Lys Ser Ala Arg His Ala His Ile Ala Val His Ala Leu His Gly
245 250 255

Thr His His Phe Gln Gly Leu Pro Phe Ala Gly Gly Ile Thr Pro Ile 260 265 270

Arg Ile Asp Arg Phe Ala Val Gln Phe Arg Leu Ile His Gly Thr Gly 275 280 285

Glu Thr Lys Arg Arg Ile Pro Pne Lys His Gln His Tyr Pro Ala Gln 290 295 300

Ser Asp Phe Asp Cys Gly Arg Ala Phe Val Val Ala Gln 305 315

<211> 648

<212> DNA

<213> Neisseria meningitidis

<220>

<221> CDS

<222> (1)..(645)

<400	> 47	7														
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ctg Leu	aat Asn	gcg Ala	oct Pro 20	tcc Ser	gaa Glu	ctg Leu	ggc Gly	aaa Lys 25	cag Gln	caa Gln	aag Lys	ttg Leu	tgg Trp 30	gcg Ala	ttt Phe	96
											gaa Glu					144
-			_		_ ~			_		_	acc Thr 60	-	_			192
											acc					240
											tac Tyr					288
											cag Glr.					336
_		_		_		_					acc Thr	_		_	atg Met	384
							Tyr								ttg Leu	432
	Thr														tcg Ser 160	480
					Ser					Tyr					ecc Pro	528

648

ggc ggc tgg cag att atc ggc aga acc gaa tta ccc ttg ttc cga gcc Gly Gly Trp Gln Ile Ile Gly Arg Thr Glu Leu Pro Leu Phe Arg Ala 180 gat ttg aat ccg ccg acc ctg ctg gcg gcg ggt gac caa gtc cgc ttt Asp Leu Asn Pro Pro Thr Leu Leu Ala Ala Gly Asp Gln Val Arg Phe 200 gtt gca gaa agg att gag cca tga Val Ala Glu Arg Ile Glu Pro 48 <210> 215 <211> <212> PRT <213> Neisseria meningitidis <400> 48 Met Arg Ile Glu Ile Thr Pro Ile Ser Glu Ser Ala Leu Val Cys Arg Leu Asn Ala Pro Ser Glu Leu Gly Lys Gln Gln Lys Leu Trp Ala Phe Aia Ala Ala Leu Gly Gln His Asp Arg Ile Glu Glu Val Val Gly Met Asn Asn Leu Thr Val Phe Thr Arg Phe Asp Thr Asp Leu Ala Thr Leu Ala Asp Glu Leu Gln Tyr Val Trp Clu His Tnr Ala Val Thr Asp His Gin Gly Lys Leu Val Glu Ile Pro Val Cys Tyr Gly Gly Glu Tyr Gly Pro Asp Leu Ala Glu Val Ala Ala Phe His Gln Thr Val Ile Ser 100 Glu Ile Val Arg Arg His Thr Ala Clm Thr Tyr Thr Val Phe Met Met Gly Phe Gln Pro Gly Phe Pro Tyr Let Gly Gly Let Pro Glu Ala Let 135 His Thr Pro Arg Arg Ala Val Pro Arg Thr Ser Val Pro Ala Gly Ser Val Gly lie Gly Gly Ser Gln Thr Gly Val Tyr Pro Phe Ala Ser Pro Gly Gly Trp Gln lie lie Gly Arg Tor Glu Leu Pro Leu Phe Arg Ala 185 Asp Leu Asn Pro Pro Thr Leu Leu Ala Ala Gly Asp Gln Val Arg Phe 200

Val Ala Glu Arg Ile Glu Pro

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185

390

	_		_	_		_	~	caa Gln 200	_	-	_	_	_			624
	-		_		_	_	~	acc Thr	_	-		_	_	_	_	672
								acc Thr								720
								gcg Ala								768
								gat Asp								816
								aaa Lys 280								864
								gtc Val								912
			gaa Glu			tga										930
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<211> 309

<212> PRT

Neisseria meningitidis

<400> 50

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Gly Arg Tyr Gly His Arg Arg Tyr Gly Ile Gly His Ala Gly Ala Met 20 \$25\$

Asp Thr Val Ala Leu Ala Ala Gly Asn Ile Leu Leu Cly Asn Asp Glu 35

Gly Thr Ala Ala Ile Glu Ile Ala Leu Gly Gly Ile Met Leu Val Phe

Glu Arg Asp Thr Pro Phe Cys Leu Thr Gly Ala Val Tyr Gln Ala Glu

Leu Asp Gly Glu Pro Val Tyr Ser Tyr Trp Arg Tyr Thr Ala Arg Lys

Gly Gln Thr Leu Lys Met Val Arg Ala Val Gln Gly Met Tyr Gly Tyr 100 105 110

Val Cys Val Ala Gly Gly Phe Asp Val Pro Glu Val Met Gly Ser Arg 115 120 125

Ser Thr Asp Leu Lys Ala Gly Phe Gly Gly His Gln Gly Arg Met Leu 130 135 140

Gln Lys Gly Asp Tyr Leu Pro Ile Gly Lys Gly Ala Gln Glu Leu Ser 145 150 155 160

Lys Val Gly Ile Ala Pro Ile Pro Phe Thr Asp Thr Ile His Leu Val 165 170 175

Pro Ser Ser Glu Tyr Ala Ala Phe Ser Glu Lys Gly Arg Leu Asn Leu 180 185 190

Glu Arg Glu Thr Trp Thr Leu Gln Ser Asp Ser Asn Arg Met Gly Tyr 195 200 205

Arg Phe Asp Gly Gln Pro Leu Thr Leu Ser Gln Pro Leu Glu Met Leu 210 215 220

Ser His Ala Val Gln Ala Gly Thr Val Gln Val Pro Pro Gly Gly Lys 225 230 235

Pro Ile Ile Leu Leu Ala Asp Ala Gln Thr Thr Gly Gly Tyr Pro Lys 245 250 255

Ile Ala Thr Val Ala Ala Ala Asp Leu Gly Arg Leu Ala Gln Val Arg 250 265 270

Phe Gly Ser Lys Val Lys Phe Lys Ile Ile Gly Leu Lys Glu Ala Thr 275 280 285

Ala Leu Arg Arg Lys Asn Gln Val Tyr Leu Asn Gln Ile Arg Arg Ile 290 295 300

Thr His Glu Ala Gly 305

<210> 51

<211> 2094

<212> DNA

<213> Neisseria meningitidis

<220>

<221> CDS

<222> (1)..(2091)

<400> 51

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10 15

ttc gcc tct gga ttc tgc gcc ctg att tac cag gtc agc tgg cag agg 96
Phe Ala Ser Gly Phe Cys Ala Leu Ile Tyr Gln Val Ser Trp Gln Arg
25

ctt Leu	cta Leu	ttc Phe 35	agt Ser	cac His	ata Ile	ggt Gly	atc Ile 40	gat Asp	ttg Leu	agt Ser	tcg Ser	att Ile 45	act Thr	gtc Val	att Ile	144
att Ile	tct Ser 50	gta Val	ttt Phe	atg Met	gt <i>c</i> Val	ggc 55	ttg Leu	ggt Gly	gta Val	ggt Gly	gcg Ala 60	tat Tyr	ttc Phe	ggt Gly	gga Gly	192
egc Arg 65	att Ile	gct Ala	gac Asp	cgt Arg	ttt Phe 70	cct Pro	tca Ser	agt Ser	atc Ile	atc Ile 75	ccc Pro	ctg Leu	ttt Phe	tgc Cys	atc Ile 80	240
gct Ala	gaa Glu	gta Val	tcc Ser	atc Ile 85	ggt	ctg Leu	ttc Phe	ggt Gly	ttg Leu 90	gta Val	agc Ser	agg Arg	ggt Gly	ctg Leu 95	att Ile	288
tcc Ser	ggc	ttg Leu	999 Gly 100	cat His	ct: Leu	tta Leu	gtt Val	gag Glu 105	gct Ala	gat Asp	ttg Leu	CCC Pro	atc Ile 110	atc Ile	gct Ala	336
gct Ala	gcc Ala	aat Asn 115	ttc Phe	ctc Leu	tta Leu	ttg Leu	ctg Leu 120	cct Leu	cct Pro	acc Thr	tt: Phe	atg Met 125	atg Met	ggc Gly	gcg Ala	384
acc Tnr	ttg Leu 130	ccc Pro	rer.	ctg Leu	acc	tgt Cys 135	ttt Phe	ttt Phe	aac Asn	cgg Arg	ааа Lys 140	ata Ile	cat Hıs	aat Asn	gtt Val	432
ggo Gly 145	gag Glu	tc: Ser	atc Ile	gly.	acc Tnr 150	tta Leu	tat	TII Phe	ttc Pne	aac Asn 155	act Thr	rtg Leu	g1;	gcg Ala	gca Ala 160	480
ese Leu	gga	ccg Ser	Leu	gcc Ala 165	gcc	gcc	gas Glu	Pne	ttr Pne 170	tac Tyr	geo Val	tt: Phe	ttt Phe	acc Trr 175	ieu Leu	528
									Pne					got Ala		576
tca Ser	gta Val	tgc Cys 195	೧೩ತ	gtt Val	aca Tnr	gaa Glu	agg Arg 100	atg Met	Yab	ata ïle	gtg	aac Asn 205	act	aaa Lys	510 ccd	62 4
		Ser					Lei					Gly		ttg Leu		672
ttg Let 225	Gly	ata Ile	gaa Glu	gto Val	ttg Leu 230	. Trp	gta Val	agg Arg	atg Met	ttt Phe 235	Ser	tto Pne	gca	gca Ala	cag Gln 240	726
tc: Ser	gtg Val	est Pro	cag Glr	gca Ala 245	Pne	tca Ser	ttt Phe	act Thr	. ctt Leu 250	. Ala	tat Tyr	ttt Phe	ctg Leu	acc Tnr 255	ggt Gly	768
ato Ile	gco Ala	gtc Val	gg Gly 260	/ Ala	tat Tyr	tt: Phe	gge Gly	aaa Lys 265	: Ars	gatt GIL	tgc Cys	cgc Arg	ago Ser 270		ttt Phe	816

gtt Val	gat Asp	att Ile 275	ccc Pro	ttt Phe	atc Ile	ejy aaa	cag Gln 280	tgc Cys	ttc Phe	ttg Leu	tgg Trp	gcg Ala 285	ggt Gly	att Ile	gcc Ala	864
gac Asp	ttt Phe 290	ttg Leu	att Ile	ttg Leu	ggt Gly	gct Ala 295	gcg Ala	tgg Trp	ttg Leu	ttg Leu	acg Thr 300	ggt Gly	ttt Phe	tcc Ser	ggc	912
ttc Phe 305	gtc Val	cac His	cac His	gcc Ala	ggt Gly 310	atc Ile	ttc Phe	att Ile	acc Thr	ctg Leu 315	tct Ser	gcc Ala	gtc Val	gtc Val	aga Arg 320	960
gly 999	ttg Leu	att Ile	ttc Phe	ccg Pro 325	ctc Leu	gta Val	cac His	cat His	gtg Val 330	ggt Gly	acg Thr	gat Asp	ggc	aac Asn 335	aaa Lys	1008
tcc Ser	gga Gly	cga Arg	cag Gln 340	gtt Val	tcc Ser	aat Asn	gtt Val	tat Tyr 345	ttc Pne	gcc Ala	aac Asn	gtt Val	gcc Ala 350	ggc	agt Ser	1056
gca Ala	ttg Leu	ggt Gly 355	ccg Pro	gtc Val	ctt Leu	atc Ile	ggc Gly 360	ttt Phe	gtg Val	ata Ile	ctt Leu	gat Asp 365	ttc Phe	ttg Leu	tcc Ser	1104
acc Thr	caa Gln 370	cag Gln	att Ile	tac Tyr	ctg Leu	ctc Leu 375	atc Ile	tg: Cys	ttg Leu	att Ile	tet Ser 380	gct Ala	gct Ala	gts Val	ect Pro	1152
ttg Leu 385	ttt Pne	tgt Cys	aca Trr	ctg Leu	tto Pne 390	caa Glm	aaa Lys	agt Ser	Ten	395 Arg Cga	ctg	aat Asn	gca Ala	gtg Val	tog Ser 400	1200
															Asp	1248
															aac Asn	1196
															gtt Val	1344
tat Tyr	999 Gly 450	Ala	aat Asn	gta Val	tac Tyr	gac Asp 455	Gly	gca Ala	tac Tyr	aat Asn	acc Thr 460	Asp	gta Val	tto Pne	aat Asn	1392
	Val					Arg					Pro				Ser 480	1440
ggo	ata Ile	cgc Arg	cgc	att Ile 485	Pne	gto Val	gtt Val	gga Gly	ttg Leu 490	Ser	aca Tnr	gg: Gly	tog Ser	TYP 495	gcg Ala	1488
cgc Arg	gto Val	ttg Lev	tct Ser	Ala	att Ile	ccg Pro	gaa Glu	atg Met	Glr	tcg Ser	ats Met	ato : Ile	gtt Val	. Ala	ggaa Glu	1536

atc a																1584
ecg o																1632
aaa t Lys : 545																1680
aat a Asn :																1728
gaa : Glu !				_	-		_				_	_			_	1776
atg 1 Met 1	rtr Phe	aat Asn 595	acc Thr	acg Thr	cac His	agc Ser	ccg Pro 600	cat Hıs	gc: Ala	ttt Phe	gct Ala	acc Thr 605	gcc Ala	gta Val	cac His	1824
agt a Ser :	att Ile 610	ccc Pro	tat Tyr	gca Ala	<u>l</u> àr rac	agc Arg €15	tat Tyr	83 A 888	cat His	atg Met	gta Val 620	gtc Val	Gly ggc	tog Ser	gca Ala	1872
acc of Thr 1 625	ccg Pro	gta Val	gtt Val	ttc Pne	est Pro 630	aat Asn	aaa Lys	gaa Glu	ctg Leu	oto Leu 635	aag Lys	caa Gln	cgt Arg	ctc Leu	tcc Ser 640	1920
ogg :																1968
gtg (Val)																2016
acg (2064
gta (Val (gaa Glu 690	tac Tyr	aaa Lys	tac	GTA	aga Arg 695	G1;	att Ile	taa							2094

<210> 52

<211> 697

<212> PRT

<213> Neisseria meningitidis

<400> 52

Met Asn Ser Thr Ala Ser Lys Thr Leu Lys Gly Leu Ser Leu Val Phe 1 5 10 15

Phe Ala Ser Gly Phe Cys Ala Leu .Ile Tyr Gln Val Ser Trp Gln Arg 20 $$\rm 25$ $\rm 30$

- Leu Leu Phe Ser His Ile Gly Ile Asp Leu Ser Ser Ile Thr Val Ile 35 40
- Ile Ser Val Phe Met Val Gly Leu Gly Val Gly Ala Tyr Phe Gly Gly 50 55
- Arg Ile Ala Asp Arg Phe Pro Ser Ser Ile Ile Pro Leu Phe Cys Ile 65 70 75 80
- Ala Glu Val Ser Ile Gly Leu Phe Gly Leu Val Ser Arg Gly Leu Ile 85 90 95
- Ser Gly Leu Gly His Leu Leu Val Glu Ala Asp Leu Pro Ile Ile Ala 100 105 110
- Ala Ala Asn Phe Leu Leu Leu Leu Pro Thr Phe Met Met Gly Ala 115 120 125
- Thr Leu Pro Leu Leu Thr Cys Phe Phe Asn Arg Lys Ile His Asn Val 130 135 140
- Gly Glu Ser Ile Gly Thr Leu Tyr Phe Phe Asn Thr Leu Gly Ala Ala 145 150 155 160
- Leu Gly Ser Leu Ala Ala Glu Phe Phe Tyr Val Phe Phe Tnr Leu 165 170 175
- Ser Gln Thr Ile Ala Leu Thr Ala Cys Phe Acn Leu Leu Ile Ala Ala 185 190
- Ser Val Cys Cys Val Thr Glu Arg Met Asp Ile Val Asn Thr Lys Pro 195 200 205
- Ash Thr Ser Leu Ile Tyr Met Leu Ser Phe Leu Ser Gly Leu Leu Ser 210 220
- Leu Gly Ile Glu Val Leu Trp Val Arg Met Phe Ser Phe Ala Ala Glm 225 230 235
- Ser Val Pro Gln Ala Phe Ser Pne Thr Leu Ala Tyr Pne Leu Thr Gly 245 250 255
- Ile Ala Val Gly Ala Tyr Phe Gly Lys Arg Ile Cys Arg Ser Arg Phe 260 270
- Val Asp Ile Pro Phe Ile Gly Gin Cys Phe Leu Trp Ala Gly Ile Ala 275 280
- Asp Phe Leu Ile Leu Gly Ala Ala Trp Leu Leu Thr Gly Phe Ser Gly 290 295 300
- Phe Val His His Ala Gly Tle Phe Tle Thr Leu Ser Ala Val Val Arg
- Gly Leu Ile Phe Pro Leu Val His His Val Gly Thr Asp Gly Asn Lys 325 330 335
- Ser Gly Arg Gln Val Ser Asn Val Tyr Phe Ala Asn Val Ala Gly Ser 340 345 350

- Ala Leu Gly Pro Val Leu Ile Gly Phe Val Ile Leu Asp Phe Leu Ser 355 360 365
- Thr Gln Gln Ile Tyr Leu Leu Ile Cys Leu Ile Ser Ala Ala Val Pro 370 375 380
- Leu Phe Cys Thr Leu Phe Gln Lys Ser Leu Arg Leu Asn Ala Val Ser 385 390 395
- Val Ala Val Ser Leu Met Phe Gly Ile Leu Met Phe Leu Leu Pro Asp 405 410 415
- Ser Val Phe Gln Asn Ile Ala Asp Arg Pro Asp Arg Leu Ile Glu Asn 420 425 430
- Lys His Gly Tle Val Ala Val Tyr His Arg Asp Gly Asp Lys Val Val 435 440 445
- Tyr Gly Ala Asn Val Tyr Asp Gly Ala Tyr Asn Thr Asp Val Phe Asn 450 455 460
- Ser Val Asn Gly Ile Glu Arg Ala Tyr Leu Leu Pro Ser Leu Lys Ser 465 470 475 480
- Gly Ile Arg Arg Ile Phe Val Val Gly Leu Ser Thr Gly Ser Trp Ala 485 490 495
- Arg Val Leu Ser Ala Ile Pro Glu Met Gln Ser Met Ile Val Ala Glu 500 505 510
- Ile Asn Pro Ala Tyr Arg Ser Leu Ile Ala Asp Giu Pro Gln Ile Ala 515 525
- Pro Leu Leu Gln Asp Lys Arg Val Glu Ile Val Leu Asp Asp Gly Arg 530 535 540
- Lys Trp Leu Arg Arg His Pro Asp Glu Lys Phe Asp Leu Ile Leu Met 545 550 555
- Asn Thr Trp Tyr Trp Arg Ala Tyr Ser Tnr Asn Leu Leu Ser Ala 565 570 575
- Glu Phe Leu Lys Gln Val Gln Ser His Leu Thr Pro Asp Gly Tle Val 580 585 590
- Met Phe Asn Thr His Ser Pro His Ala Phe Ala Thr Ala Val His 595 600 605
- Ser Ile Pro Tyr Ala Tyr Arg Tyr Gly His Met Val Val Gly Ser Ala 610 615 620
- Thr Pro Val Val Phe Pro Asn Lys Glu Leu Leu Lys Gln Arg Leu Ser 625 630 635
- Arg Leu Ile Trp Pro Glu Ser Gly Arg His Val Phe Asp Ser Ser Thr 645 650 655
- Val Asp Ala Ala Gln Lys Val Val Ser Arg Met Leu Ile Gln Met 660 670

Thr Glu Pro Ser Ala Gly Ala Glu Val Ile Thr Asp Asp Asn Met Ile 675 680 685

Val Glu Tyr Lys Tyr Gly Arg Gly Ile 690 695

<210> 53

<211> 1040

<212> PRT

<213> Neisseria meningitidis

<400> 53

Cys Leu Gly Gly Gly Gly Gly Thr Ser Ala Pro Asp Phe Asn Ala Gly
1 5 10 15

Gly Thr Gly Ile Gly Ser Asn Ser Arg Ala Thr Thr Ala Lys Ser Ala 20 25 30

Ala Val Ser Tyr Ala Gly Ile Lys Asn Glu Met Cys Lys Asp Arg Ser 35 40 45

Met Leu Cys Ala Gly Arg Asp Asp Val Ala Val Thr Asp Arg Asp Ala 50 55

Lys Ile Asn Ala Pro Pro Pro Asn Leu His Thr Gly Asp Phe Thr Asn 65 70 75 80

Pro Asn Asp Ala Tyr Lys Asn Leu Ile Asn Leu Lys Pro Ala Ile Glu 85 90 95

Ala Gly Tyr Thr Gly Arg Gly Val Glu Val Gly Ile Val Asp Thr Gly 100 105 110

Glu Ser Val Gly Ser Ile Ser Phe Pro Glu Leu Tyr Gly Arg Lys Glu 115 120 125

His Gly Tyr Asn Glu Asn Tyr Lys Asn Tyr Thr Ala Tyr Met Arg Lys 130 135 140

Glu Ala Pro Glu Asp Gly Gly Gly Lys Asp Ile Lys Ala Ser Phe Asp 145 150 155 160

Asp Glu Ala Val Ile Glu Thr Glu Ala Lys Pro Thr Asp Ile Arg His 165 170 175

Val Lys Glu Ile Gly His Ile Asp Val Val Ser His Ile Ile Gly Gly
180 185 190

Arg Ser Val Asp Gly Arg Pro Ala Gly Gly Ile Ala Pro Asp Ala Thr 195 200 205

Leu His Ile Met Asn Thr His Asp Gly Thr Lys Asn Glu Ile Met Ser 210 225

Ala Ala Ile Arg Asn Ala Trp Val Lys Leu Gly Glu Arg Gly Val Arg 225 230 235

- Ile Val Asn Asn Ser Phe Gly Thr Thr Ser Arg Ala Gly Thr Ala Asp 245 250 255
- His Phe Gln Ile Ala Asn Ser Glu Glu Gln Tyr Arg Gln Ala Leu Leu 260 265 270
- Ala Tyr Ser Gly Gly Asp Lys Thr Asp Glu Gly Ile Arg Leu Met Gln 275 280 285
- Gln Ser Asp Tyr Gly Asn Leu Ser Tyr His Ile Arg Asn Lys Asn Met 290 295 300
- Leu Phe Ile Phe Ser Ala Ser Asn Asp Ala Gln Ala Gln Pro Asn Thr 305 310 315 320
- Leu Thr Leu Leu Pro Phe Tyr Glu Lys Asp Ala Gln Lys Gly Ile Ile 325 330 335
- Thr Val Ala Gly Val Asp Arg Ser Gly Glu Lys Phe Asn Gly Ser Asn 340 345 350
- His Cys Gly Ile Thr Ala Met Trp Cys Leu Ser Ala Pro Tyr Glu Ala 355 \$360\$
- Ser Val Arg Phe Thr Arg Thr Asn Pro Ile Gln Ile Ala Gly Thr Ser 370 375 380
- Phe Ser Ala Pro Ile Val Thr Gly Thr Ala Ala Leu Leu Leu Gln Lys 385 390 395 400
- Tyr Pro Trp Met Ser Asn Asp Asn Leu Arg Thr Thr Leu Leu Thr Thr 405 410 415
- Ala Gin Asp Ile Gly Ala Val Gly Val Asp Ser Lys Phe Gly Trp Gly 420 425 430
- Leu Leu Asp Ala Gly Lys Ala Met Asn Gly Pro Ala Ser Phe Pro Phe 435 440 445
- Gly Asp Phe Thr Ala Asp Thr Lys Gly Thr Ser Asp Ile Ala Tyr Ser 450 460
- Phe Arg Asn Asp IIe Ser Gly Thr Gly Gly Leu IIe Lys Lys Gly Gly 465 470 475 480
- Ser Gln Leu Gln Leu His Gly Asn Asr. Thr Tyr Thr Gly Lys Thr Ile 485 490
- Ile Glu Gly Gly Ser Leu Val Leu Tyr Gly Asn Asn Lys Ser Asp Met 500 500 510
- Arg Val Glu Thr Lys Gly Ala Leu Ile Tyr Asn Gly Ala Ala Ser Gly 515 520 525
- Gly Ser Leu Asn Ser Asp Gly Ile Val Tyr Leu Ala Asp Thr Asp Arg
 530 535 540
 - Ser Gly Ala Asn Glu Thr Val His Ile Lys Gly Asp Leu Gln Leu Gly 545 550 . 555 560

- Gly Glu Gly Thr Leu Tyr Thr Arg Leu Gly Lys Leu Leu Lys Val Asp 565 570 570
- Gly Thr Ala Met Thr Gly Gly Lys Leu Tyr Met Ser Ala Arg Gly Lys 580 585 590
- Gly Ala Gly Tyr Leu Asn Arg Thr Gly Gln Arg Val Pro Phe Leu Ser 595 600 605
- Ala Ala Lys Ile Gly Arg Asp Tyr Ser Phe Phe Thr Asn Ile Glu Thr 610 615 620
- Asp Gly Gly Leu Leu Ala Ser Leu Asp Ser Val Glu Lys Thr Ala Gly 625 630 635
- Ser Glu Gly Asp Thr Leu Ser Tyr Tyr Val Arg Arg Gly Asn Ala Ala 645 650 655
- Arg Thr Ala Ser Ala Ala Ala His Ser Ala Pro Ala Gly Leu Lys His 660 665 670
- Ala Val Glu Gln Gly Gly Ser Asn Leu Glu Asn beu Met Val Glu Leu 675 680 685
- Asp Ala Ser Glu Ser Ser Ala Thr Pro Glu Thr Val Glu Thr Ala Ala 690 695 700
- Ala Asp Arg Thr Asp Met Pro Gly Ile Arg Pro Tyr Gly Ala Thr Phe 705 710 715 720
- Arg Ala Ala Ala Val Gln His Ala Asn Ala Ala Asp Gly Val Arg
 725 730 730
- Ile Phe Asn Ser Leu Ala Ala Thr Val Tyr Ala Asp Ser Thr Ala Ala 740 745 750
- His Ala Asp Met Gln Gly Arg Arg Leu Lys Ala Val Ser Asp Gly Leu 755 760 765
- Asp His Asn Ala Thr Gly Leu Arg Val Ile Ala Gln Thr Gln Gln Asp 770 780
- Gly Gly Thr Trp Glu Gln Gly Gly Val Glu Gly Lys Met Arg Gly Ser
 785 790 795 800
- Thr Glr Thr Val Gly Ile Ala Ala Lys Thr Gly Glu Asn Thr Thr Ala 805 810 815
- Ala Ala Thr Leu Gly Met Gly His Ser Thr Trp Ser Glu Asn Ser Ala 820 825 830
- Asn Ala Lys Thr Asp Ser Ile Ser Leu Phe Ala Gly Ile Arg His Asp 835 840 845
- Ala Gly Asp Ile Gly Tyr Leu Lys Gly Leu Phe Ser Tyr Gly Arg Tyr 850 860
- Lys Asn Ser Ile Ser Arg Ser Thr Gly Ala Asp Glu His Ala Glu Gly 865 870 875

Ser Val Asn Gly Thr Leu Met Gln Leu Gly Ala Leu Gly Gly Val Asn 885 890 895

Val Pro Phe Ala Ala Thr Gly Asp Leu Thr Val Glu Gly Gly Leu Arg 900 905 910

Tyr Asp Leu Lys Gln Asp Ala Phe Ala Glu Lys Gly Ser Ala Leu 915 920 925

Gly Trp Ser Gly Asn Ser Leu Thr Glu Gly Thr Leu Val Gly Leu Ala 930 935 940

Gly Leu Lys Leu Ser Gln Pro Leu Ser Asp Lys Ala Val Leu Phe Ala 945 950 955 960

Thr Ala Gly Val Glu Arg Asp Leu Asn Gly Arg Asp Tyr Thr Val Thr 965 970 975

Gly Gly Phe Thr Gly Ala Thr Ala Ala Thr Gly Lys Thr Gly Ala Arg 980 985 990

Asn Met Pro His Thr Arg Leu Val Ala Gly Leu Gly Ala Asp Val Glu
995 1000 1005

Phe Gly Asn Gly Trp Asn Gly Leu Ala Arg Tyr Ser Tyr Ala Gly Ser 1010 1015 1020

Lys Gln Tyr Gly Asn His Ser Gly Arg Val Gly Val Gly Tyr Arg Phe 1025 1030 1035 1040

<210> 54

<211> 858

<212> DNA

<213> Neisseria gonorrhoeae

<220>

<221> CDS

<222> (1)..(855)

<400> 54

atg tot gaa gaa aaa ttg aaa atg agt tto gag oca acc gta ato gaa 48 Met Ser Glu Glu Lys Leu Lys Met Ser Phe Glu Pro Thr Val Ile Glu 1 5 10 15

Cat ttg ggt gta aag atg tat tcg cac act gtt cct gcg att gcc gag 96
His Leu Gly Val Lys Met Tyr Ser His Thr Val Pro Ala Ile Ala Glu
20 30

ttg ata gcg aat gcc tac gat gca tgt gct acg gaa gtg gaa gtt agg 144 Leu Ile Ala Asn Ala Tyr Asp Ala Cys Ala Thr Glu Val Glu Val Arg 35 40

tta ttc gat aaa ccg gag cat aaa atc gtt att aaa gat aat ggc ata 192
Leu Phe Asp Lys Pro Glu His Lys Ile Val Ile Lys Asp Asn Gly Ile
50 60

				gat Asp												240
			_	gaa Glu 85			_		-	_		_			-	288
				ctt Leu												336
				act Thr												384
				att												432
				gtt Val												480
	_		_	acg Thr 165								-				528
				cgt Arg												576
				aac Asn												624
				gtt Val					_				_	_		672
				tca Ser												720
agc Ser	gga Gly	tta Leu	ata Ile	caa Gln 245	ggt ggt	aag Lys	ttc Phe	att Ile	aca Thr 250	acg Thr	gaa Glu	aaa Lys	cct Pro	tta Leu 255	aag Lys	768
				ggt Gly												816
				ttc Phe									taa			858

<210> 55

<211> 285

<212> PRT

<213> Neisseria gonorrhoeae

<400> 55

Met Ser Glu Glu Lys Leu Lys Met Ser Phe Glu Pro Thr Val Ile Glu

1 5 10 15

His Leu Gly Val Lys Met Tyr Ser His Thr Val Pro Ala Ile Ala Glu 20 25 30

Leu Ile Ala Asn Ala Tyr Asp Ala Cys Ala Thr Glu Val Glu Val Arg

Leu Phe Asp Lys Pro Glu His Lys Ile Val Ile Lys Asp Asn Gly Ile 50 55 60

Gly Met Ser Phe Asp Glu Ile Asn Asp Phe Tyr Leu Arg Ile Gly Arg 65 70 75 80

Asn Arg Arg Glu Glu Lys Gln Ala Ser Pro Cys Gly Arg Ile Pro Thr 85 90 95

Gly Lys Lys Gly Leu Gly Lys Leu Ala Leu Phe Arg Leu Gly Asn Lys 100 105 110

Ile Glu Ile Ser Thr Ile Gln Gly Asn Glu Arg Val Thr Phe Thr Leu 115 120 125

Asp Tyr Ala Glu Ile Lys Lys Ser Glu Arg Ile Tyr Gln Pro Glu Phe 130 135 140

Gln Lys Glu Ser Val Lys Pro Asn Thr Glu Asn Gly Thr Thr Ile Thr 145 150 155 160

Leu Thr Glu Leu Thr Lys Lys Gln Gly Tyr Pro Leu Asp Asn Tyr Val

Gly His Leu Ser Arg Leu Phe Asp Phe Pro Ala Gln Asp Phe Lys Ile 180 185 190

Lys Val Ser Leu Asn Gly Ser Glu Pro Arg Ile Ile Asp Gly Asn Leu 195 200 205

Lys Tyr Asn Leu Val Thr Pro Gin Phe Glu Trp Glu Tyr Gln Asp Leu 210 215 220

Ala Thr Asn Ile Ser Ser Leu Ser Ser Lys Phe Glu Gln Tyr Glu Tyr 225 230 240

Ser Gly Leu Ile Gln Gly Lys Phe Ile Thr Thr Glu Lys Pro Leu Lys 245 250 255

Asn Asn Met Lys Gly Ile Thr Leu Phe Ala Asn Gly Arg Met Val Asn 260 265 270

Met Pro Glu Phe Phe Thr Asp Ser Glu Ser Ser His Phe 275 280 285

<210> 56

<211> 1575

<212> DNA

<213> Neisseria gonorrhoeae

<220>

<221> CDS

<222> (1)..(1572)

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gcc Ala	agc Ser	gaa Glu	atc 11e 20	gcc Ala	tat Tyr	cgc Arg	tt Phe	gta Val 25	ttc Phe	gga Gly	att Ile	gaa Glu	acc Thr 30	tta Leu	ccg Pro	96
gct Ala	gca Ala	aaa Lys 35	atg Met	gcg Ala	gaa Glu	acg Thr	ttt Phe 40	gcg Ala	ctg Leu	aca Thr	ttt Phe	atg Met 45	att Ile	gct Ala	gcg Ala	144
ctg Leu	tat Tyr 50	ctg Leu	tt: Phe	gcg Ala	cgt Arg	tat Tyr 55	aag Lys	gct Ala	tcg Ser	cgg Arg	ctg Leu 60	ctg Leu	att Ile	gcg Ala	gtg Val	192
ttt Phe 65	ttc Phe	gcg Ala	ttc Phe	agc Ser	atg Met 70	att Ile	gcc Ala	aac Asn	aat Asn	gtg Val 75	cat His	tac Tyr	gcg Ala	gtt Val	tat Tyr 80	240
caa Gln	agc Ser	tgg Trp	atg Met	acg Thr 85	ggt	att Ile	aac Asn	tat Tyr	tgg Trp 90	ctg Leu	atg Met	ctg Leu	aaa Lys	gag Glu 95	gtt Val	288
acc Thr	gaa Glu	gtc Val	ggc Gly 100	Ser	gcg Ala	ggc	gcg Ala	tcg Ser 105	atg Met	ttg Leu	gat Asp	aag Lys	ttg Leu 110	Trp	ctg Leu	336
cct Pro	gct Ala	ttg Leu 115	Trp	gly ggc	gtg Val	gcg Ala	gaa Glu 120	gtc Val	atg Met	ttg Leu	ttt Phe	tgc Cys 125	agc Ser	ctt Leu	gcc Ala	384
aag Lys	tto Phe	arc	cgt Arg	aag Lys	acg Thr	cat His	Phe	tct Ser	gcc	gat Asp	ata Ile 140	e Leu	ttt Phe	gco Ala	ttc Phe	432
cta Leu 145	Met	g cto Lev	ato 1 Met	g att	ttc Phe	: Val	cgt Arg	tcg Ser	tto Phe	gao Asp 155	Thi	g aaa C Lys	caa Glr	ı gaçı ı Glu	g cac His 160	480
ggt Gly	ati	t tog e Ser	g ccc	c aaa Lys 165	Pro	aca Thr	tac Tyr	ago Ser	2 cgc Arg	g Ile	aaa Lys	a gco s Ala	aat Asi	tat 1 Ty:	ttc Phe	528
ago Sei	tt. Ph	c ggi e Gl	t tai y Ty: 18	r Phe	t gto e Val	: Gl ⁾	g egg Ærg	g gtg g Val	LLe	g cc	g ta o Ty:	t caq r Gli	g tto 19	u Pne	: gat e Asp	576
tt: Le:	a ag u Se	c aag	g at s Il	c cc	t gtg o Val	g tto l Phe	aaa E Ly:	a caq s Gl:	g cc n Pr	t gc o Al	t cc a Pr	a ago	c aa r Ly	a at	c ggg e Gly	624

195 200 205

caa	aac	agt	att	caa	aat	atc	gtc	cta	att	atq	qqc	qaa	agc	qaa	aqc	672
Gln	ĞÎy 210	Ser	Ile	Gln	Asn	Ile 215	Val	Leu	Ile	Met	Gly 220	Glu	Ser	Glu	Ser	
							ggt Gly									720
							gat Asp									768
							gca Ala									816
							ttg Leu 280									864
							gag Glu									912
							atg Met									960
							cag Gln									1008
							aag Lys									1056
							ttt Phe 360									1104
												Lys			Gly	1152
	Ala					Lys					Ile				gac Asp 400	1200
										Gln					Gly	1248
				Āla					His					Arg	caa Gln	1296
gat Asp	ato	tac Tyr	aat Asn	caa Gln	ggo Gly	acg Thr	gtg Val	cag Gln	ccc Pro	gac Asp	ago Ser	tat Tyr	att Ile	gto Val	rcct Pro	1344

440 445 435 ctg gtt ttg tac agc ccg gat aag gcc gtg caa cag gct gcc aac cag Leu Val Leu Tyr Ser Pro Asp Lys Ala Val Gln Gln Ala Ala Asn Gln 455 get tit geg eet tge gag att gee tte eat eag eag ett tea aeg tte Ala Phe Ala Pro Cys Glu Ile Ala Phe His Gln Gln Leu Ser Thr Phe 470 1488 ctg att cac acg ttg ggc tac gat atg ccg gtt tca ggt tgt cgc gaa Leu Ile His Thr Leu Gly Tyr Asp Met Pro Val Ser Gly Cys Arg Glu 490 gge teg gta aca gge aac etg att acg gge gat gea gge age ttg aac Gly Ser Val Thr Gly Asn Leu Ile Thr Gly Asp Ala Gly Ser Leu Asn 505 1575 att cgc aac ggc aag gcg gaa tat gtt tat ccg caa taa Ile Arg Asn Gly Lys Ala Glu Tyr Val Tyr Pro Gln 515 520

<210> 57

<211> 524

<212> PRT

<213> Neisseria gonorrhoeae

<400> 57

Met Lys Lys Ser Leu Phe Val Leu Phe Leu Tyr Ser Ser Leu Leu Thr 1 5 10 15

Ala Ser Glu Ile Ala Tyr Arg Phe Val Phe Gly Ile Glu Thr Leu Pro 20 25 30

Ala Ala Lys Met Ala Glu Thr Phe Ala Leu Thr Phe Met Ile Ala Ala 35 40 45

Leu Tyr Leu Phe Ala Arg Tyr Lys Ala Ser Arg Leu Leu Ile Ala Val 50 55

Phe Phe Ala Phe Ser Met Ile Ala Asn Asn Val His Tyr Ala Val Tyr 65 70 75 80

Gln Ser Trp Met Thr Gly Ile Asn Tyr Trp Leu Met Leu Lys Glu Val 85 90 95

Thr Glu Val Gly Ser Ala Gly Ala Ser Met Leu Asp Lys Leu Trp Leu 100 105 110

Pro Ala Leu Trp Gly Val Ala Glu Val Met Leu Phe Cys Ser Leu Ala 115 120 125

Lys Phe Arg Arg Lys Thr His Phe Ser Ala Asp Ile Leu Phe Ala Phe 130 135 140

Leu Met Leu Met IIe Phe Val Arg Ser Phe Asp Thr Lys Gln Glu His 145 150 155 160

Gly Ile Ser Pro Lys Pro Thr Tyr Ser Arg Ile Lys Ala Asn Tyr Phe

				165					170					175	
Ser	Phe	Gly	Tyr 180	Phe	Val	Gly	Arg	Val 185	Leu	Pro	Tyr	Gln	Leu 190	Phe	Asp
Leu	Ser	Lys 195	Ile	Pro	Val	Phe	700 Tàs	Gln	Pro	Ala	Pro	Ser 205	Lys	Ile	Gly
Gln	Gly 210	Ser	Ile	Gln	Asn	Ile 215	Val	Leu	Ile	Met	Gly 220	Glu	Ser	Glu	Ser
Ala 225	Ala	His	Leu	Lys	Leu 230	Phe	Gly	Tyr	Gly	Arg 235	Glu	Thr	Ser	Pro	Phe 240
Leu	Thr	Arg	Leu	Ser 245	Gln	Ala	Asp	Phe	Lys 250	Pro	Ile	Val	Lys	Gln 255	Ser
Tyr	Ser	Ala	Gly 260	Phe	Met	Thr	Ala	Val 265	Ser	Leu	Pro	Ser	Phe 270	Phe	Asn
Val	Ile	Pro 275	His	Ala	Asn	Gly	Leu 280	Glu	Gln	Ile	Ser	Gly 285	GŢĀ	Asp	Thr
Asn	Met 290	Phe	Arg	Leu	Ala	Lys 295	Glu	Gln	Gly	Tyr	Glu 300	Thr	Tyr	Phe	Tyr
Ser 305	Ala	Gln	Ala	Glu	Asn 310	Gln	Met	Ala	Ile	Leu 315	Asn	Leu	Ile	Gly	Lys 320
Lys	Trp	Ile	Asp	His 325	Leu	Ile	Gln	Pro	Thr 330	Gln	Leu	Gly	Tyr	Gly 335	Asn
Gly	Asp	Asn	Met 340	Pro	Asp	Glu	Lys	Leu 345	Leu	Pro	Leu	Phe	Asp 350	Lys	Ile
Asn	Leu	Gln 355	Gln	Gly	Arg	His	Phe 360	Ile	Val	Leu	His	Gln 365	Arg	Gly	Ser
His	Ala 370	Pro	Tyr	Gly	Ala	Leu 375	Leu	Gln	Pro	Gln	Asp 380	Lys	Val	Phe	Gly
Glu 385		Asp	Ile				Tyr					His	Lys	Thr	Asp 400
Gln	Met	Ile	Gln	Thr 405	Val	Phe	Giu	Gln	Leu 410	Gln	Lys	Gln	Pro	Asp 415	Gly
Asn	Trp	Leu	Phe 420	Ala	Tyr	Thr	Ser	Asp 425		Gly	Gln	Tyr	Val 430	Arg	Gln
Asp	Ile	Tyr 435		Gln	Gly	Thr	Val 440	Gln	Pro	Asp	Ser	Tyr 445		Val	Pro
Leu	Val 450		Tyr	Ser	Pro	Asp 455		Ala	Val	Gln	Gln 460		Ala	Asn	Gln
Ala 465		Ala	Pro	Cys	Glu 470		Ala	Phe	His	Gln 475		Leu	Ser	Thr	Phe 480

Leu Ile His Thr Leu Gly Tyr Asp Met Pro Val Ser Gly Cys Arg Glu

Gly Ser Val Thr Gly Asn Leu Ile Thr Gly Asp Ala Gly Ser Leu Asn 500 505 510

Ile Arg Asn Gly Lys Ala Glu Tyr Val Tyr Pro Gln 515 520

<210> 58

<211> 1314

<212> DNA

<213> Neisseria gonorrhoeae

<220>

<221> CDS

<222> (1)..(1311)

<400> 58

atg ctg acg ttt atc gga ttg ctg att atc ggg gtc atc gta tgg ctg

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1 5 10 15

tig ctg acg gaa aaa gtg tog ccc atc atc gca tra atc tig gtg ccg 96 Leu Leu Thr Clu Lys Val Ser Pro Ile Ile Ala Leu Ile Leu Val Pro

Ctg att ggg gcg ttg ctg gcg ggg ttt gat gta tcc caa tta aaa gaa 144
Leu Ile Gly Ala Leu Leu Ala Gly Phe Asp Val Ser Gln Leu Lys Glu
35 40 45

the tar tog ggo ggo acg aaa tog gtg acg cag att gtg att atg tot 192
Phe Tyr Ser Gly Gly Thr Lys Ser Val Thr Gln Ile Val Ile Met Phe
50

atg tit too att tig tit tit gga atc atg aac gat gtg ggg cig tit 240 Met Phe Ser Ile Leu Phe Phe Cly Ile Met Asn Asp Val Gly Leu Phe 65 75 80

ogt oog atg ata gge ggt ttg att aag otg act ogg ggt aat ate gtg 288 Arg Pro Met Ile Gly Gly Leu Ile Lys Leu Thr Arg Gly Asn Ile Val

gsa gtg agt gtg ggg acg gtc ttg gtg tcg gtg gtg gca cag ttg gac 336 Ala Val Ser Val Gly Thr Val Leu Val Ser Val Val Ala Gln Leu Asp

999 909 990 909 acg acg ttt tta tcg gtc gtc ccc gcc ctt ttg ccg 384 Gly Ala Gly Ala Thr Thr Phe Leu Ser Val Val Pro Ala Leu Leu Pro 115 120 125

Ctt tac aag ogt dig cat atg aat oot tac dig dig tit tig dig dig. 43: Leu Tyr Lys Arg Leu His Met Ash Pro Tyr Leu Leu Phe Leu Leu Leu 130 135

act too ago gog gog cta ato aac ctt ttg cog egg gog egg cog ato 480 Thr Ser Ser Ala Gly Leu Ile Asn Leu Leu Pro Arg Gly Gly Pro Ile 145 150 155 160

The first that the first that the first than the fi

GJA aaa	cgg Arg	gtt Val	gca Ala	agc Ser 165	gtg Val	ttg Leu	gly	gca Ala	gat Asp 170	gtg Val	ggc Gly	gaa Glu	ttg Leu	tat Tyr 175	aaa Lys	528
cct Pro	ttg Leu	ttg Leu	acg Thr 180	gtg Val	caa Gln	att Ile	atc Ile	ggt Gly 185	gtg Val	gtg Val	ttt Phe	atc Ile	ctt Leu 190	gtg Val	ctg Leu	576
tcc Ser	ctg Leu	ttt Phe 195	ttg Leu	ggt Gly	gtg Val	cgt Arg	gaa Glu 200	aaa Lys	agg Arg	cgg Arg	att Ile	gtc Val 205	cgg Arg	gag Glu	ttg Leu	624
ggc	gcg Ala 210	ttg Leu	ccc Pro	gcc Ala	gtg Val	gcg Ala 215	gat Asp	ttg Leu	ata Ile	aag Lys	ccg Pro 220	gcg Ala	cct Pro	ttg Leu	tcg Ser	672
gaa Glu 225	gaa Glu	gaa Glu	caa Gln	aaa Lys	ttg Leu 230	gcg Aìa	cgt Arg	ecg Pro	aaa Lys	ctg Leu 235	ttt Phe	tgg Trp	tgg Trp	aat Asn	gtc Val 240	720
ctg Leu	ctg Leu	ttt Phe	ttg Leu	gcg Ala 245	gcg Ala	atg Met	agc Ser	ctg Leu	ctt Leu 250	ttt Phe	tcg Ser	ggc	atc Ile	ttc Phe 255	eeg Pro	768
ccg Pro	Gly	tat Tyr	gta Val 260	Phe	atg Met	ctg Leu	gct	gta Ala 263	acg Thr	gcg Ala	gcg Ala	ttg Leu	ctt Leu 270	ttg Leu	aat Asn	816
tac Tyr	agc Arg	agc Ser 275	Pro	cag Gln	gaa Glu	cag Gln	atg Met 280	Gju gag	cgg Arg	att	tat Tyr	gcc Ala 285	cac Hıs	gcc Ala	Gly	864
Gly	gcg Ala 290	Val	atg Met	atg Met	gcg Ala	100 Ser 295	I≟e	att	ttg Leu	geg Ala	gca Ala 300		acg Thr	ttt Phe	trg Leu	912
999 Gly 305	Tle	ttg Leu	rys aag	gly ggc	geg Ala 310	Gly	atg Met	ttg Leu	gac Asp	gcg Ala 315	. lle	tcc Ser	aaa Lys	gac Asp	ctt Leu 320	960
gtg Val	cat His	ato	t Ctg	9 009 1 Pro 325	Asp	gcg Ala	ttg Leu	ctg Le	cot Pro 330	Tyr	tev	cat His	att	gco Ala 333	atc	1008
ggt Gly	gtg Val	ı itg Lev	99t Gl;	/ Ile	ccg Pro	t ott	Glu	: EE9 : Leu 349	. Val	tto Let	g agt	acg Thr	gac Asg 350	Ala	tat Tyr	1056
tat Ty:	tto Phe	gga Gly 355	Lev	g tt: 1 Phs	cog Pro	; att	geg Val 360	Giv	cas Glr	g att 1 Ile	t aco	teg Ser 365	Glr	g gcg 1 Ala	g ggc	1104
gtt Val	gca L Ala 370	l Pro	gaa Glu	a gcg	g gca a Ala	375 375	r Tyr	s gag	g atg a Met	g ttg Le:	g ato 1 Ile 389	e Gly	agt / Set	i at:	gre val	1152
ggt G1) 385	y Thi	ttt r Phe	i gt: e Val	t acq	g ccg r Pro 390	Le	teg 1 Se:	g dog r Pro	g gct	t ttg a Le	u Tr	g ato p Mei	g 99'	t tt: y Le	g ggt u Gly 400	1200

ttg gcg aaa ttg tcg atg ggc aaa cac atc cgt tat tcg ttt ttc tgg 1248 Leu Ala Lys Leu Ser Met Gly Lys His Ile Arg Tyr Ser Phe Phe Trp 405 410 415

gcg tgg ggt ttg tcg ctg gcg ata ttg gtc agt tcg ata gcg gca gga 1296 Ala Trp Gly Leu Ser Leu Ala Ile Leu Val Ser Ser Ile Ala Ala Gly 420 425 430

atc gtg cct ctg ccg taa Ile Val Pro Leu Pro 435 1314

<210> 59

<211> 437

<212> PRT

<213> Neisseria gonorrhoeae

<400> 59

Met Leu Thr Phe Ile Gly Leu Leu Ile Ile Gly Val Ile Val Trp Leu 1 5 10 15

Leu Leu Thr Glu Lys Val Ser Pro Ile Ile Ala Leu Ile Leu Val Pro 20 25 30

Leu Ile Gly Ala Leu Leu Ala Gly Phe Asp Val Ser Glm Leu Lys Glu 45

Phe Tyr Ser Gly Gly Thr Lys Ser Val Thr Gln Ile Val Tie Met Phe 50 60

Met Pae Ser Ile Leu Phe Pae Gly lle Met Ash Asp Val Gly Leu Phe 65 70 75

Arg Pro Met Ile Gly Gly Leu Ile Lys Leu Thr Arg Gly Asn Ile Val 85 90 95

Ala Val Ser Val Gly Thr Val Leu Val Ser Val Val Ala Cln Leu Asp 100 105 110

Gly Ala Gly Ala Thr Thr Phe Leu Ser Val Val Pro Ala Leu Leu Pro 115 120

Leu Tyr Lys Arg Leu His Met Asn Pro Tyr Leu Leu Phe Leu Leu 130 140

Thr Ser Ser Ala Gly Leu Ile Asn Leu Leu Pro Arg Gly Gly Pro Ile 145 150 155

Gly Arg Val Ala Ser Val Leu Gly Ala Asp Val Gly Glu Leu Tyr Lys 165 170 175

Pro Leu Deu Thr Val Glm Ile Ile Gly Val Val Phe Ile Leu Val Leu 180 185 190

Ser Leu Phe Leu Gly Val Arg Glu Lys Arg Arg Ile Val Arg Glu Leu 195 200 205

Gly Ala Leu Pro Ala Val Ala Asp Leu Ile Lys Pro Ala Pro Leu Ser 210 215 220 Glu Glu Glu Gln Lys Leu Ala Arg Pro Lys Leu Phe Trp Trp Asn Val 225 230 235 240

Leu Leu Phe Leu Ala Ala Met Ser Leu Leu Phe Ser Gly Ile Phe Pro 245 250 255

Pro Gly Tyr Val Phe Met Leu Ala Ala Thr Ala Ala Leu Leu Leu Asn 260 265 270

Tyr Arg Ser Pro Gln Glu Gln Met Glu Arg Ile Tyr Ala His Ala Gly
275 280 285

Gly Ala Val Met Met Ala Ser Ile Ile Leu Ala Ala Gly Thr Phe Leu 290 295 300

Gly Ile Leu Lys Gly Ala Gly Met Leu Asp Ala Ile Ser Lys Asp Leu 305 310 315

Val His Ile Leu Pro Asp Ala Leu Leu Pro Tyr Leu His Ile Ala Ile 325 330 335

Gly Val Leu Gly Ile Pro Leu Glu Leu Val Leu Ser Thr Asp Ala Tyr 340 345

Tyr Phe Gly Leu Phe Pro Ile Val Glu Gln Ile Thr Ser Gln Ala Gly 355 360 365

Val Ala Pro Glu Ala Ala Gly Tyr Ala Met Leu Ile Gly Ser Ile Val 370 380

Gly Thr Phe Val Thr Pro Leu Ser Pro Ala Leu Trp Met Gly Leu Gly 385 390 395

Leu Ala Lys Leu Ser Met Gly Lys His Ile Arg Tyr Ser Phe Phe Trp 405 416 415

Ala Trp Gly Leu Ser Leu Ala Ile Leu Val Ser Ser Ile Ala Ala Gly 420 425 430

Ile Val Pro Leu Pro 435

<210> 60

<211> 1155

<212> DNA

<213> Neisseria gonorrhoeae

<220>

<221> CDS

<222> (1)..(1152)

<400> 60

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act tat ctg tat caa aag ccc aag ctc ttt aaa gga gcg gtt cgg aat 9

Thr	Tyr	Leu	Tyr 20	Gln	Lys	Pro.	Lys	Leu 25	Phe	Lys	Gly	Alą	Val 30	Arg	Asn	·* • .
	gaa Glu															144
	cca Pro 50		-	_	_											192
	aaa Lys															240
	cgt Arg															288
	tta Leu															336
	cgt Arg		_	-	_		-							-		384
	ctt Leu 130															432
	gat Asp															480
	gcc Ala		_			_		_		_					-	528
	gat Asp					_			_	-				Leu		576
	ggt Gly															624
	CTC Leu 210															
	ggc										Lys					
_	agt Ser	_	_		_			_		Glu					Arg	
atc	aac	gat	act	Scc	gca	caa	att	gct	gcc	atg	att	gcc	gac	ccc	gto	816

Ile	Asn	Asp	Thr 260	Ala	Ala	Gln	Ile	Ala 265	Ala	Met	Ile	Ala	Asp 270	Pro	Val	··· .
aat Asn	tat Tyr	gaa Glu 275	gcc Ala	ttc Phe	agt Ser	gaa Glu	gac Asp 280	ttt Phe	ctc Leu	ggc Gly	aaa Lys	gaa Glu 285	cgt Arg	acc Thr	gat Asp	864
acc Thr	gct Ala 290	ttt Phe	cat His	ctc Leu	gaa Glu	cag Gln 295	ttc Phe	gcg Ala	aat Asn	ccc Pro	aac Asn 300	gct Ala	act Thr	ccg Pro	ctt Leu	912
tca Ser 305	gac Asp	gac Asp	gtc Val	agg Arg	ttg Leu 310	aga Arg	tta Leu	aat Asn	gcc Ala	aat Asn 315	aat Asn	ttg Leu	gat Asp	acg Thr	ttg Leu 320	960
gaa Glu	aag Lys	gga Gly	tat Tyr	ttg Leu 325	att Ile	ggg Gly	aat Asn	ggg Gly	atg Met 330	aag Lys	ata Ile	agc Ser	gta Val	gat Asp 335	gag Glu	1008
ttg Leu	Gly	aaa Lys	aaa Lys 340	Val	tta Leu	gaa Glu	cac His	atc Ile 345	ggt Gly	aag Lys	aat Asn	gaa Glu	ccg Pro 350	tta Leu	ttg Leu	1056
ttg Leu	aaa Lys	aat Asn 355	Leu	ctg	gtt Val	aac Asn	ttc Phe 360	Asn	cag Gln	gca Ala	aaa Lys	cat His 365	gaa Glu	gaa Glu	gtt Val	1104
agg Arg	aag Lys 370	Leu	ato Tle	tat Tyr	cag Gln	ttg Leu 375	Ile	gag Glu	tta Leu	gat Asp	ttt Phe 380	: Leu	gaa Glu	att Ile	ttg Leu	1152
tga	ı															1155

<210> 61

<211> 384

<212> PRT

<213> Neisseria gonorrhoeae

<400> 61
Met Gly Ile His Leu Asp Phe Gly Ile Ser Pro Lys Thr Phe Arg Gln
1 5 10 15

Thr Tyr Leu Tyr Gln Lys Pro Lys Leu Phe Lys Gly Ala Val Arg Asn 20 25 30

Leu Glu Ala Ala Ser Cys Lys Tyr Ile Asn Glu Ile Tyr Gln Arg Ala 35 40 45

Asp Pro Thr Ala Pro Leu Phe His Leu Arg Lys Lys Gly Ala Ile Val 50 55 60

Pro Lys Glu Glu Tyr Val Glu Ser Phe Asp Asp Leu Gly Lys Thr Arg 65 70 75 80

Tyr Arg Phe Ile Lys Ser Val Ile Tyr Clu His Met Lys Asn Gly Ala 85 90 95

Ser Leu Val Tyr Asn His Ile Asn Asn Glu Pro Phe Ser Asp His Ile 100 105 110 Ala Arg Gln Val Ala Arg Phe Ala Gly Ala His Thr Ile Val Ser Gly
115 120

Tyr Leu Ala Phe Gly Ser Asp Glu Ser Tyr Lys Asn His Trp Asp Thr 130 140

Arg Asp Val Tyr Ala Ile Gln Leu Phe Gly Lys Lys Arg Trp Gln Leu 145 150 155

Thr Ala Pro Asp Phe Pro Met Pro Leu Tyr Met Gln Gln Thr Lys Asp 165 170 175

Thr Asp Ile Ser Ile Pro Glu His Ile Asp Met Asp Ile Ile Leu Glu
180 185 190

Ala Gly Asp Val Leu Tyr Ile Pro Arg Gly Trp Trp His Arg Pro Ile 195 200 205

Pro Leu Gly Cys Glu Thr Phe His Phe Ala Val Gly Thr Phe Pro Pro 210 215 220

Asn Gly Tyr Asn Tyr Leu Glu Trp Leu Met Lys Lys Phe Pro Thr Ile 225 230 235 240

Glu Ser Leu Arg His Ser Phe Ser Asp Trp Glu Gln Asp Arg Thr Arg 245 250 255

Tie Asn Asp Thr Ala Ala Glr Ile Ala Ala Met Ile Ala Asp Pro Val 260 265 270

Ash Tyr Glu Ala Phe Ser Glu Asp Phe Leu Gly Lys Glu Arg Thr Asp 275 280 285

Thr Ala Phe His Leu Glu Gln Phe Ala Asn Pro Asn Ala Thr Pro Leu 290 295 300

Ser Asp Asp Val Arg Leu Arg Leu Asn Ala Asn Asn Leu Asp Thr Leu 305 315 320

Glu Lys Gly Tyr Leu Ile Gly Asn Gly Met Lys Ile Ser Val Asp Glu 325 330 335

Let Gly Lys Lys Val Let Glu His Ile Gly Lys Asn Glu Pro Let Let 340 348 350

Leu Lys Asn Leu Leu Val Asn Phe Asn Gln Ala Lys His Glu Glu Val 355 360 365

Arg Lys Leu Ile Tyr Gln Leu Ile Glu Leu Asp Phe Leu Glu Ile Leu 370 380

<210> 62

<211> 717

<212> DNA

<213> Neisseria meningitidis

<221> CDS

<222> (1)..(714)

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cgc caa a Arg Gln T	cc agc hr Ser 20	ctg acg Leu Thr	ggt a Gly L	aa gtg ys Val 25	att d	etg ac Leu Th	a cga nr Arg	ccg ! Pro 1 30	ttg Leu	tca Ser	96
ttt tcc c Phe Ser L	ta tgg eu Trp 35	acg aca Thr Thr	Phe A	ca tog la Ser 40	ata i	tct go Ser Al	eg tta La Leu 45	ttg (Leu :	att Ile	atc Ile	144
ctg ttt t Leu Phe L 50	tg ata eu Ile	ttt ggt Pne Gly	aac t Asn T 55	at acg Yr Thr	cga (Lys Tr	ca aca or Thr	gtg : Val :	gag Glu	gga Gly	192
caa att t Gln Ile L 65	ta cct eu Pro	gca tog Ala Ser 70	Gly V	gta atc /al Ile	agg (gtg ta Val Ty 75	at gca yr Ala	ccg Pro	gat Asp	acg Thr 80	240
ggg aca a Gly Thr I	itt aca le Thr	gcg aaa Ala Lys 85	ttc g	gtg gaa Val Glu	gat Asp 90	gga ga Gly Gl	aa aag lu Lys	gtt Val	aag Lys 95	gct Ala	288
ggc gac a	ag cta Lys Leu 100	Pne Ala	; ctt t i Leu S	tog acc Ser Thr 105	tca Ser	ogt ti Arg Pi	tc ggc he Gly	gca Ala 110	gga Gly	gat Asp	336
age gtg o Ser Val (eag cag Eln Glr	cag tto	ı Lys :	acg gag Tnr Glu 120	gca Ala	gtt t Val L	tg aag eu Lys 125	aaa Lys	acg Thr	ttg Leu	384
gca gaa d Ala Glu (130	ag gaa 31n Glu	t ctg gg: 1 Leu Gl;	egt o Arg 1	otg aag Leu bys	ctg Leu	Ile H	ac ggg is Gly 40	aat Asn	gaa Glu	acg Tnr	432
cgc agc o Arg Ser 1 145	ctt aaa Leu Lys	a gca ac s Ala Th 15	r Val	gaa cgt Glu Arg	tig Leu	gaa a Glu A 155	ac cag sn Gln	gaa Glu	ctc Leu	cat His 160	480
att tog (Ile Ser (caa caq Gln Glr	g ara ga n Ile As 165	c ggt p Gly	cag aaa Gln Lys	agg Arg 170	cgc a Arg I	itt aga He Arg	ctt Leu	gcg Ala 175	gaa Glu	528
gaa atg : Glu Met :	ttg caq Leu Gli 180	n Lys Ty	t egt r Arg	ttc cta Phe Lev 18:	ı Ser	gcc a Ala A	at gat Asn Asp	gca Ala 190	g:g Val	cca Pro	5 76
aaa caa Lys Gln	gaa atq Glu Mer 195	g atg aa t Met As	t gtc n Val	aag go: Lys Al. 200	a gag a Clu	ctt t Leu I	ita gag Leu Glu 205	ı Gln	aaa Lys	gcc Ala	624
aaa ctt Lys Leu 210	gat go Asp Al	c tac co a Tyr Ar	c cga g Arg 215	gaa ga Glu Gl	a gtc u Val	Gly 1	ctg ctt Leu Lev 220	cag ıGln	gaa Glu	atc Ile	672
cgc acg c Arg Thr G 225			r Leu							a	717

<211> 238

<212> PRT

<213> Neisseria meningitidis

<400> 63

Met Asn Arg Pro Lys Gln Pro Phe Phe Arg Pro Glu Val Ala Val Ala 1 5 10 15

Arg Gln Thr Ser Leu Thr Gly Lys Val Ile Leu Thr Arg Pro Leu Ser 20 25 30

Phe Ser Leu Trp Thr Thr Phe Ala Ser Ile Ser Ala Leu Leu Ile Ile 35 40 45

Leu Phe Leu Ile Phe Gly Asn Tyr Thr Arg Lys Thr Thr Val Glu Gly 50 55 60

Gln Ile Leu Pro Ala Ser Gly Val Ile Arg Val Tyr Ala Pro Asp Thr
65 70 75 80

Gly Thr Ile Thr Ala Lys Phe Val Glu Asp Gly Giu Lys Val Lys Ala 85 90 95

Gly Asp Lys Leu Phe Ala Leu Sor Thr Ser Arg Phe Gly Ala Gly Asp 100 105 110

Ser Val Gln Gln Leu Lys Thr Glu A'a Val Leu Lys Lys Thr Leu 115 120 125

Ala Glu Glu Leu Gly Arg Leu Lys Leu Ile His Gly Asn Olu Thr 130 140

Arg Ser Leu Lys Ala Thr Val Glu Arg Leu Glu Asm Glm Glu Leu His 145 150 155 160

Ile Ser Gln Gln Ile Asp Gly Gln Lys Arg Arg Ile Arg Leu Ala Glu 165 170 175

Glu Met Leu Gln Lys Tyr Arg Phe Leu Ser Ala Asn Asp Ala Val Pro 180 185

Lys Gln Glu Met Met Asn Val Lys Ala Glu Leu Leu Glu Gln Lys Ala 195 206 205

Lys Leu Asp Ala Tyr Arg Arg Glu Glu Val Gly Leu Leu Gln Glu Ile 210 215 220

Arg Thr Gln Asn Leu Thr Leu Ala Ser Leu Pro Gln Ala Ala 225 235

<210> 64

<211> 690

<212> DNA

<213> Neisseria meningitidis

<221> CDS

<222> (1)..(687)

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	ctg Leu															144
	ctt Leu 50															192
	atg Met															240
	ata Ile															288
	ttg Leu															336
	ccc Pro															384
	cgt Arg 130															432
	gtc Val															480
	ttg Leu									Lys						528
	ctc Leu			Ile					Pro					Tyr	ggt Gly	576
			Pro					Met					Asp		cta Leu	624
His	gag Glu 210	aaa Lys	cgg Arg	cgg Arg	ctg Leu	tac Tyr 215	gaa Glu	tgg Trp	gta Val	ttg Leu	gag Glu 220	ccg Pro	att Ile	tac Tyr	agt Ser	672
atg Met 225	tcg Ser	ggc Gly	agg Arg	ttg Leu	taa											690

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<210> 65
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<211> 229

<212> PRT

<213> Neisseria gonorrhoeae

<400> 65

Met Met Asn Val Glu Ala Glu Leu Leu Glu Gln Lys Ala Lys Leu Asp 1 5 10 15

Asn Leu Thr Leu Ala Ser Leu Pro Lys Arg His Glu Thr Glu Gln Ser 35 40 45

Gln Leu Glu Arg Thr Met Ala Asp Ile Ser Gln Glu Val Leu Asp Phe 50 55 60

Glu Met Arg Ser Glu Gln Ile Ile Arg Ala Gly Arg Ser Gly Tyr Ile 65 70 75 80

Ala Ile Pro Asn Val Glu Val Gly Arg Gln Val Asp Pro Ser Lys Leu 85 90 95

Leu Leu Ser Ile Val Pro Glu Arg Thr Glu Leu Tyr Ala His Leu Tyr 100 103 110

lie Pro Ser Ser Ala Ala Gly Phe Ile Lys Pro Lys Asp Lys Val Val 125

Leu Arg Tyr Gin Ala Tyr Pro Tyr Gin Lys Phe G'y Leu Ala Ser Gly 130 135 140

Ser Val Val Ser Val Ala Lys Thr Ala Leu Gly Arg Gln Glu Leu Ser 145 150 155 160

Gly Leu Gly Met Val Ser Ser Asp Leu Ala Lys Ser Asn Glu Pro Val

Tyr Leu Val Lys Ile Lys Pro Asp Lys Pro Thr Ile Tnr Ala Tyr Gly 180 185 190

Glu Glu Lys Pro Leu Gln Ile Gly Met Thr Leu Glu Ala Asp Ile Leu 195 200 205

His Glu Lys Arg Arg Leu Tyr Glu Trp Val Leu Glu Pro Ile Tyr Ser 210 215 220

Met Ser Gly Arg Leu 225

<210> 66

<211> 924

<212> DNA

<213> Neisseria gonorrhoeae

<221> CDS <222> (1)..(921)

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aat aat ti Asn Asn Pl							
age cat go Ser His A							
tca ggg co Ser Gly As							
toc gtc as Ser Val As 65	ac ctc gct sn Leu Ala						
gtg cgc ga Val Arg G	aa cgc cto lu Arg Lei 83	Asn Ile	-		-	-	
ttt ggc ga Phe Gly As	ac ago ago sp Ser Aro 100	gat ttt Asp Pne	gto gaa Val Glu 105	aaa atg Lys Met	gaa gog Glu Ala	cac gcc His Ala 110	Gly ggc 336
Lys Leu Le	tt tot tto eu Ser Phe 15						
tto att ad Phe Ile Ti 130	cc ctc coc hr Leu Pro	ttg ttg Leu Leu 135	ege ges Arg Ala	cac gcc His Ala	cgc tat Arg Tyr 140	ttc ggc Phe Gly	aaa 432 Lys
ctc gca c Leu Ala Le 145	tg att cat eu Ile His	ttt gac Phe Asp 150	gog cac Ala His	acc gac Thr Asp 155	Thr Tyr	gac aac Asp Asn	ggc 480 Gly 160
	ac gac cac yr Asp His	Gly Thr					Gly
	ac ccg tco sp Pro Ser 180			. Ile Gly			

						gtg Val 200					624
						cgt Arg					672
		-		_		gac Asp	-	-		_	720
						gta Val					768
						ctg Leu					816
						tct Ser 280					864
						ttg Leu					912
	aag Lys	_	tga								924
210>	> 6	7									

<2

<211> 307

<212> PRT

<213> Neisseria gonorrhoeae

<400> 67

Met Gln Tyr Ser Thr Leu Ala Gly Gln Thr Asp Asn Ser Leu Val Ser

Asn Asn Phe Gly Phe Leu Arg Leu Pro Leu Asn Phe Met Pro Tyr Glu

Ser His Ala Asp Trp Val Ile Thr Glv Val Pro Tyr Asp Met Ala Val

Ser Gly Arg Ser Gly Ala Arg Phe Gly Pro Glu Ala Ile Arg Arg Ala

Ser Val Asn Leu Ala Trp Glu His Arg Arg Phe Pro Trp Thr Phe Asp 65 70 75 80

Val Arg Glu Arg Leu Asn Ile Ile Asp Cys Gly Asp Leu Val Phe Ser

Phe Gly Asp Ser Arg Asp Phe Val Glu Lys Met Glu Ala His Ala Gly 100 105

Lys Leu Leu Ser Phe Gly Lys Arg Cys Leu Ser Leu Gly Gly Asp His

Phe Ile Thr Leu Pro Leu Leu Arg Ala His Ala Arg Tyr Phe Gly Lys 130 135 140

Leu Ala Leu Ile His Phe Asp Ala His Thr Asp Thr Tyr Asp Asn Gly 145 150 150

Ser Glu Tyr Asp His Gly Thr Met Phe Tyr Thr Ala Pro Lys Glu Gly 165 170 175

Leu Ile Asp Pro Ser Arg Ser Val Gln Ile Gly Ile Arg Thr Glu His 180 185 190

Ser Lys Lys Leu Pro Phe Thr Val Leu Ser Ala Pro Lys Val Asn Glu 195 200 205

Asp Ser Val Glu Glu Thr Val Arg Lys Ile Lys Glu Thr Val Gly Asn 210 220

Met Pro Val Tyr Leu Thr Phe Asp Ile Asp Cys Leu Asp Pro Ser Phe 225 230 235

Ala Pro Gly Thr Gly Thr Pro Val Cys Gly Gly Leu Ser Ser Asp Arg 245 250 255

Ala Leu Lys Ile Leu Arg Gly Leu Thr Asp Leu Asp Ile Val Gly Met 260 265 270

Asp Val Val Glu Val Ala Pro Ser Tyr Asp Gln Ser Asp Ile Thr Ala 275 280 285

Leu Ala Gly Ala Thr Ile Ala Leu Glu Met Leu Tyr Leu Cln Gly Ala 290 300

Lys Lys Asp 305

<210> 68

<211> 1404

<212> DNA

<213> Neisseria meningitidis

<220>

<221> CDS

<222> (1)..(1401)

<400> 68

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1 5 10 15

tgc etg aca etg acg ece tat ttg caa cat gaa eta ttt teg get atg 96 Cys Leu Thr Leu Thr Pro Tyr Leu Gln His Glu Leu Phe Ser Ala Met 20 25 30

ada too tat tit too aaa tat ato ota ooo git toa oit tit aco tig 144

Lys	Ser	Tyr 35	Phe	Ser	Lys	Tyr .	Ile 40	Leu	Pro	Val	Ser	Leu 45	Phe	Thr	Leu	
cca Pro	cta Leu 50	tcc Ser	ctt Leu	tcc Ser	cca Pro	tcc Ser 55	gtt Val	tcg Ser	gct Ala	ttt Phe	acg Thr 60	ctg Leu	cct Pro	gaa Glu	gca Ala	192
tgg Trp 65	cgg Arg	gcg Ala	gcg Ala	cag Gln	caa Gln 70	cat His	tcg Ser	gct Ala	gat Asp	ttt Phe 75	caa Gln	gcg Ala	tcc Ser	cat His	tac Tyr 80	240
cag Gln	cgt Arg	gat Asp	gca Ala	gtg Val 85	cgc Arg	gca Ala	cgg Arg	caa Gln	caa Gln 90	caa Gln	gcc Ala	aag Lys	gcc Ala	gca Ala 95	ttc Phe	288
ctt Leu	ccc	cat Hís	gta Val 100	tcc Ser	gcc Ala	aat Asn	gcc Ala	agc Ser 105	tac Tyr	cag Gln	cgc Arg	cag Gln	ccg Pro 110	cca Pro	tcg Ser	336
att Ile	tct Ser	tcc Ser 115	acc	cgc Arg	gaa Glu	aca Thr	cag Gln 120	gga Gly	tgg	agc Ser	gtg Val	cag Gln 125	gtg Val	gga Gly	caa Gln	384
acc Thr	tta Leu 130	ttt Phe	gac Asp	get Ala	gcs Ala	aaa Lys 135	ttt Phe	gca Ala	caa Gln	tac Tyr	egc Arg 140	caa Gln	agc Ser	agg Arg	ttc Phe	432
gat Asp 145	acg Thr	cag Gln	gct	gca Ala	gaa Glu 150	cag Gln	egt Arg	ttc Pne	gat Asp	gcg Ala 155	gca Ala	cgc Arg	gaa Glu	gaa Glu	ttg Leu 160	480
ctg Leu	t t.g Leu	aaa Lys	gtt Val	gec Ala 165	gaa Glu	agt Ser	cat Cyr	tto Pne	aac Asn 170	gtt Val	cta Leu	ctc Leu	agc Ser	oga Arg 175	gac Asp	528
acc	gtt Val	gcc	gcc Ala 180	His	gcg	geg Ala	gaa Glu	aaa Lys 185	Glu	gct Ala	tat Tyr	gcc Ala	cag Glm 190	. Glm	gta Val	576
agg Arg	cag Gln	gcg Ala	Gln	get Ala	. tta Leu	ttc Phe	aat Asn 200	Lys	ggt Gly	got Ala	gcc Ala	acc Thi 205	Ala	ctg Leu	gat Asp	624
att	cac His	: Glu	gcc Ala	aaa Lys	gco Ala	ggt Gly 213	Tyr	gac Asp	: aat : Asn	goo Ala	cto Lev 220	ı Ala	caa Glr	ı gaa ı Glu	atc Tle	672
gcc Ala 225	. Val	ttg Leu	g gct	gag Glu	g aaa 1 Lys 230	Gln	acc Thi	nat Tyt	gaa Glu	a aad 1 Asi 235	n Gli	; ttg 1 Lev	aac LASI	gac Asp	tac Tyr 240	720
acc Thi	gad As <u>r</u>	c ctg	gat 1 Asp	245	c Lys	caa Glm	ato Lile	gaç e Gl:	g gcc 2 Ala 250	a Ile	a gat e Asi	acc Thr	ge Ala	aac Asr 258	ctg Leu	768
tt <u>s</u> Lei	ı Ala	a cgo	tat Ty: 26	c Le	g cco	aac Lys	g cto Le	g gaa u Gli 26:	ı Arg	t ta g Ty	c agi	t cts r Lei	g ga: 1 As; 27	p Glu	tgg Trp	816
cas	â câ	c ati	c gc	c tt	a tc	c aac	22	t ca	c ga	a ta	c cg	g atq	g ca	g ca	g ctt	864

Gln	Arg	Ile 275	Ala	Leu	Ser	Asn	Asn 280	His	Glu	Tyr	Arg	Met 285	Gln	Gln	Leu	
gcc Ala	ctg Leu 290	caa Gln	agc Ser	agc Ser	gga Gly	cag Gln 295	gcg Ala	ctt Leu	cgg Arg	gca Ala	gca Ala 300	cag Gln	aac Asn	agc Ser	cgc Arg	912
	ccc Pro															960
	tct Ser															1008
	GJA ääc															1056
	aaa Lys															1104
	acc Thr 370															1152
acc Thr 385	gaa Glu	agc Ser	gly ggt	gcg	gcg Ala 390	cgt Arg	tac Tyr	caa Gln	atc	atg Met 395	gcg Ala	caa Gln	gaa Glu	cgg Arg	gtt Val 400	1200
	gaa Glu															1245
tac Tyr	gly ggc	ats	cgc Arg 420	aac Asn	ogg Arg	ctg Leu	gaa	gta Val 425	ata ile	cgg	gcg Ala	Yrd cââ	cag Gln 430	gaa Glu	gtc Val	1296
gcc Ala	caa Gln	gca Ala 435	gaa Glu	cag Gln	aaa Lys	ctg Leu	gct Ala 440	caa Gln	gca Ala	arg	tat Tyr	aaa Lys 445	ttc Phe	atg Met	ctg Leu	1344
		Leu					ĞŢ,7								gta Val	1392
	gcg Ala															1404

<211> 467

<212> PRT

<213> Neisseria meningitidis

<400> 69

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- Cys Leu Thr Leu Thr Pro Tyr Leu Gln His Glu Leu Phe Ser Ala Met 20 25 30
- Lys Ser Tyr Phe Ser Lys Tyr Ile Leu Pro Val Ser Leu Phe Thr Leu 35 40 45
- Pro Leu Ser Leu Ser Pro Ser Val Ser Ala Phe Thr Leu Pro Glu Ala 50 55 60
- Trp Arg Ala Ala Gln Gln His Ser Ala Asp Phe Gln Ala Ser His Tyr
 65 70 75 80
- GIn Arg Asp Ala Val Arg Ala Arg Gin Gln Gln Ala Lys Ala Ala Phe $85 \hspace{1cm} 90 \hspace{1cm} 95$
- Leu Pro His Val Ser Ala Asn Ala Ser Tyr Gln Arg Gln Pro Pro Ser 100 105 110
- Ile Ser Ser Thr Arg Glu Thr Gln Gly Trp Ser Val Gln Val Gly Gln
 115 120 125
- Thr Leu Phe Asp Ala Ala Lys Phe Ala Gln Tyr Arg Gln Ser Arg Phe 130 135 140
- Asp Thr Gln Ala Ala Glu Gln Arg Phe Asp Ala Ala Arg Glu Glu Leu 145 150 155 160
- Leu Leu Lys Val Ala Glu Ser Tyr Phe Asn Val Leu Leu Ser Arg Asp 165 170 175
- Thr Val Ala Ala His Ala Ala Slu Dys Glu Ala Tyr Ala Gln Gln Val 180 185
- Arg Gln Ala Gln Ala Leu Phe Asn Lys Gly Ala Ala Thr Ala Leu Asp 195 200 205
- 11e His Glu Ala Lys Ala Gly Tyr Asp Asn Ala Leu Ala Gln Glu Ile
 210 225
- Ala Val Leu Ala Clu Lys Gln Thr Tyr Glu Asn Gln Leu Asn Asp Tyr 225 230 235
- Thr Asp Leu Asp Ser Lys Gln Ile Glu Ala Ile Asp Thr Ala Asn Leu 245 250 255
- Leu Ala Arg Tyr Leu Pro Lys Leu Glu Arg Tyr Ser Leu Asp Glu Trp
 260 255 270
- Gln Arg Ile Ala Leu Ser Asn Asn His Glu Tyr Arg Met Gln Gln Leu 275 280 285
- Ala Leu Gln Ser Ser Gly Gln Ala Leu Arg Ala Ala Gln Asn Ser Arg 290 295 300
- Tyr Pro Thr Val Ser Ala His Val Gly Tyr Gln Asn Asn Leu Tyr Thr 305 310 315
- Ser Ser Ala Gln Asn Asn Asp Tyr His Tyr Arg Gly Lys Gly Met Ser 325 330 335

Val Gly Val Gln Leu Asn Leu Pro Leu Tyr Thr Gly Gly Glu Leu Ser 345 Gly Lys Ile His Glu Ala Glu Ala Gln Tyr Gly Ala Ala Glu Ala Gln Leu Thr Ala Thr Glu Arg His Ile Lys Leu Ala Val Arg Gln Ala Tyr 375 Thr Glu Ser Gly Ala Ala Arg Tyr Gln Ile Met Ala Gln Glu Arg Val Leu Glu Ser Ser Arg Leu Lys Leu Lys Ser Thr Glu Thr Gly Gln Gln Tyr Gly Ile Arg Asn Arg Leu Glu Val Ile Arg Ala Arg Gln Glu Val Ala Gln Ala Glu Gln Lys Leu Ala Gln Ala Arg Tyr Lys Phe Met Leu Ala Tyr Leu Arg Leu Val Lys Glu Ser Gly Leu Gly Leu Glu Thr Val 450 455 460 Phe Ala Glu 465 <210> 70 <211> 696 <212> DNA <213> Neisseria gonorrhoeae <220> <221> CDS <222> (1)..(693) <400> 70 atg aaa caa too goo oga ata aaa aat atg gat cag aca tta aaa aat Met Lys Gln Ser Ala Arg Ile Lys Asn Met Asp Gln Thr Leu Lys Asn aca tig ggo att igo gog ott tia god tit tgi tit ggo gog god atc Thr Leu Gly Ile Cys Ala Leu Leu Ala Phe Cys Phe Gly Ala Ala Ile goa toa ggt tat cac tig gaa tat gaa tac ggc tac cgt tat tot gcc Ala Ser Gly Tyr His Leu Glu Tyr Glu Tyr Gly Tyr Arg Tyr Ser Ala gig gge get tig get tog git gia tit tia tia tig gea ege gge Val Gly Ala Leu Ala Ser Val Val Pre Leu Leu Leu Leu Ala Arg Gly tto dog ogo git tot toa git git tha otg att tac git ggc aca acc Phe Pro Arg Val Ser Ser Val Val Leu Leu Ile Tyr Val Gly Thr Thr

75

70

gcc Ala	cta Leu	tat Tyr	ttg Leu	ccg Pro 85	gtc Val	ggc	tgg Trp	ctg Leu	tat Tyr 90	ggt Gly	gcg Ala	ect Pro	tct Ser	tat Tyr 95	cag Gln	288
ata Ile	gtc Val	ggt Gly	tcg Ser 100	ata Ile	ttg Leu	gaa Glu	agc Ser	aat Asn 105	cct Pro	gcc Ala	gag Glu	gcg Ala	cgt Arg 110	gaa Glu	ttt Phe	336
gtc Val	Gly	aat Asn 115	ctt Leu	ccc Pro	GŢÀ āāā	tcg Ser	ctt Leu 120	tat Tyr	ttt Phe	gtg Val	cag Gln	gca Ala 125	tta Leu	ttt Phe	ttc Phe	384
att Ile	Ttt Phe 130	ggc Gly	ttg Leu	aca Thr	gtt Val	tgg Trp 135	aaa Lys	tat Tyr	tgt Cys	gta Val	tct Ser 140	gtg Val	ejà aaa	gta Val	ttt Phe	432
gct Ala 145	gac Asp	gta Val	aaa Lys	aac Asn	tat Tyr 150	aaa Lys	cgt Arg	egc Arg	agc Ser	aaa Lys 155	ata Ile	tgg Trp	ctg Leu	acc Thr	ata Ile 160	480
tca Leu	ttg Leu	act Thr	ttg Leu	att Ile 1 <i>6</i> 5	ttg Leu	tcc Ser	tge Cys	gcg Ala	gtg Val 170	atg Met	gag Glu	aaa Lys	atc Ile	gcc Ala 175	Gly	528
gat Asp	rys	gat Asp	tgg Trp 180	cga Arg	gaa Glu	cct Pro	gat Asp	gcc Ala 185	Gly aac	ctg Leu	ttg Leu	ttg Leu	aat Asn 190	att Ile	ttc Phe	576
gac	Leu Ctg	tat Tyr 195	Chr rec	gac Asp	ttg Leu	got Ala	ttc Phe 200	Arg	goo Ala	gly ggc	aca Thr	ata Ile 205	rgc Cys	cgc Arg	caa Gln	624
gog Ala	ege Arg 213	cca Pro	cat His	ttt Phe	gga Gly	agt Ser 215	agc Ser	asa Lys	aaa Lys	agc Ser	gtc Val 220	aac Asn	atg Met	gca Ala	tat Tyr	672
552 520 66 3	eca Pro	act Thr	tgc Cys	ges Ala	caa Gln 230	gta Va]	taa									696

<211> 231

<212> PRT

<213> Neisseria gonorrhoeae

<400> 71

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Thr Leu Gly Ile Cys Ala Leu Leu Ala Phe Cys Pne Gly Ala Ala Ile 20 29 30

Ala Ser Gly Tyr His Leu Glu Tyr Glu Tyr Gly Tyr Arg Tyr Ser Ala 35 40 45

Val Gly Ala Leu Ala Ser Val Val Phe Leu Leu Leu Leu Ala Arg Gly 50 55 60

Phe Pro Arg Val Ser Ser Val Val Leu Leu Ile Tyr Val Gly Thr Thr

65					70					75					80
Ala	Leu	Tyr	Leu	Pro 85	Val	Gly	Trp	Leu	Tyr 90	Gly	Ala	Pro	Ser	Tyr 95	Gln
Ile	Val	Gly	Ser 100	Ile	Leu	Glu	Ser	Asn 105	Pro	Ala	Glu	Ala	Arg 110	Glu	Phe
Val	Gly	Asn 115	Leu	Pro	Gly	Ser	Leu 120	Tyr	Phe	Val	Gln	Ala 125	Leu	Phe	Phe
Ile	Phe 130	Gly	Leu	Thr	Val	Trp 135	Ľуs	Tyr	Сув	Val	Ser 140	Val	Gly	Val	Phe
Ala 145	Asp	Val	īys	Asn	Tyr 150	Lys	Arg	Arg	Ser	Lys 155	Ile	Trp	Leu	Thr	Ile 160
Leu	Leu	Thr	Leu	Ile 165	Leu	Ser	Cys	Ala	Val 170	Met	Glu	Lys	Ile	Ala 175	Gly
Asp	Lys	Asp	Trp 180	Arg	Glu	Pro	Asp	Ala 185	Gly	Leu	Leu	Leu	Asn 190	Ile	Phe
Asp	Leu	Tyr 195	Tyr	Asp	Leu	Ara	Phe 200	Arg	Ala	Gly	Thr	Ile 205	Cys	Arg	Gln
Ala	Arg 210	5ro	His	Phe	Gly	Ser 215	Ser	Lys	Lys	Ser	Val 220	Asn	Met	Ala	Tyr
Pro 225	Pro	Thr	Cys	Ala	Gln 230	Val									
<210>	7:	2													
<211>	26	607													
<212>	Dì	A													
<213>	Ne	eis	ser:	ia n	neni	git	idi	.s							
<220>															
<221>	CI	os													
<222>	(=	l).	. (26	504)											
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gaa t Glu T	ac t Yr T	yr A	ac g sp A 20	og og la A	gt go rg Al	g go la Al	a Cy	t ga 's Gl	9 99 u Gl	c at	c aaa e Lys	ccc Pro	Gly	: tct Ser	96
tac g Tyr A	rab r	ag c ys L 35	tg c eu P	ct ta ro T	ac ac yr Ti	ır Se	e co r Ar	c at	t tt e Le	g gc u Al	g gag a Glu 45	Asr	ttg Leu	gtc Val	144
aac c Asn A	gc g Ig A 50	cg g la A	ac a sp L	aa g: ys V:	al As	it to sp Le	g co	g ac	g ct r Le	g ca u Gl: 6	n Sei	tgg Trp	g ctg	ggt Gly	192

cag (Gln :	ctg Leu	att Ile	Glu gag	gga Gly	aaa Lys 70	cag Gln	gaa Glu	atc Ile	gac Asp	ttt Phe 75	cct Pro	tgg Trp	tat Tyr	ccg Pro	gcg Ala 80	240
cgg	gtg Val	gtg Val	tgc Cys	cac His 85	gat Asp	att Ile	ctg Leu	Gly 999	cag Gln 90	acc Thr	gcg Ala	ttg Leu	gtg Val	gat Asp 95	ttg Leu	288
gca Ala	ggt Gly	ctg Leu	cgc Arg 100	gat Asp	gcg	att Ile	gcc Ala	gaa Glu 105	aaa Lys	ggc Gly	ggc Gly	gat Asp	cct Pro 110	gcc Ala	aaa Lys	336
gtg Val	aat Asn	ccg Pro 115	gtg Val	gtg Val	caa Gln	acc Thr	cag Gln 120	ctc Leu	atc Ile	gtc Val	gac Asp	cac His 125	tcg Ser	ctg Leu	gcg Ala	384
gtg Val	gaa Glu 130	tgc Cys	ggc Gly	Gly ggc	tac Tyr	gac Asp 135	ccc Pro	gat As p	gcg Ala	ttc Phe	cgc Arg 140	aaa Lys	aac Asn	cgc Arg	gaa Glu	432
atc Ile 145	gaa Glu	gac Asp	aga Arg	cgt Arg	aac Asn 150	gaa Glu	gac Asp	cgt	ttc Phe	cac His 155	ttc Phe	atc Ile	aac Asn	tgg Trp	aca Thr 160	480
aaa Lys	acc	gct Ala	ttt Pne	gaa Glu 165	aat Asn	gtg Vál	gac Asp	gtg Val	att Ile 170	Pro	geg Ala	Gly	aac Asn	ggc Gly 175	TTE	528
atg Met	cac His	caa Gln	ato Ile 180	Asn	Cta Leu	gaa Glu	aaa Lys	atg Met 185	tcg Ser	ccc Pro	gto Val	gtc Val	caa Glr 190	g:c Val	aaa Lys	576
aac Asn	ggc	grg Val 195	Ala	ttc Phe	ccc Pro	gat Asp	acc Thr 200	tgs	gtc Val	ggo	acg Tnr	gat Asp 205	Ser	cac H1s	acg Thr	624
cca	cac His 210	Val	gat Asp	geg Ala	ctg Leu	ggo Gly 215	. Val	att Ile	tee Ser	gtg Val	gg: Gly 220	· Va.	ggc Gly	gga gga	ttg / Leu	672
gaa Glu 225	Ala	gaa Glu	a acc	e gea r Val	atg Met 230	Let	gga Gly	ogo Arg	gog Ala	tco Ser 239	: Met	g atg	r cgo : Arg	cto Lei	9 CCC 1 Pro 240	720
gat Asp	att Ile	gta Val	e gga	e get y Val 249	l Gli	r ctg	; aac 1 Asī	gg«	: aas : Lys 250	a Arg	g aag g Lys	g gog s Ala	g ggc	: att	acg Thr	768
gcg Ala	acc Thi	ga: Asj	t at: p Il: 26	e Val	g ttg l Lei	g gca Ala	a cts	g act i Thi 26!	c Gli	g tt: u Phe	t ctq	g cgo	270 270	s GT:	a cgc u Arg	815
gt <u>e</u> Val	gt: Val	2 999 1 G1; 27	y Al	g tt a Pn	t gto e Val	gaa Gl	a tto E Pro 280	e Ph	e gg	y Gl	n er. B æð	y Ala 28	a Ar	a ag g Se	c ctg r Leu	864
rct Se:	at: 11:	e Gl	c ga y As	c cg p Ar	g Al	g ac a Th	r Il	t to e Se	c aa r As	c at n Me	g ac t Th 30	r Pr	g ga: o Gl	g tt u Ph	e Gly	912

gcg Ala 305	act Thr	gcc Ala	gcg Ala	atg Met	ttc Phe 310	gct Ala	att Ile	gat Asp	gag Glu	caa Gln 315	acc Thr	att Ile	gat Asp	tat Tyr	ttg Leu 320	960
aaa Lys	ctg Leu	acc Thr	gga Gly	cgc Arg 325	gac Asp	gac Asp	gcg Ala	cag Gln	gtg Val 330	aaa Lys	ttg Leu	gtg Val	gaa Glu	acc Thr 335	tac Tyr	1008
gcc Ala	aaa Lys	acc Thr	gca Ala 340	ggc Gly	ttg Leu	tgg Trp	gca Ala	gat Asp 345	gcc Ala	ttg Leu	aaa Lys	acc Thr	gcc Ala 350	gtt Val	tat Tyr	1056
ecg Pro	cgc Arg	gtt Val 355	ttg Leu	aaa Lys	ttt Phe	gat Asp	ttg Leu 360	agc Ser	agc Ser	gta Val	acg Thr	cgc Arg 365	aat Asn	atg Met	gca Ala	1104
ggc Gly	ccg Pro 370	agc Ser	aac Asn	ccg Pro	cac His	gcg Ala 375	cgt Arg	ttt Phe	gcg Ala	acc Thr	gcc Ala 380	gat Asp	ttg Leu	gcc Ala	gly	1152
											gac Asp					1200
gac	ggt Gly	gca Ala	gtg Val	att Ile 405	att	gcc Ala	gcg Ala	att Ile	act Thr 410	tcc Ser	tgt Cys	acc Thr	aat Asn	act Thr 415	tcc Ser	1248
aat Asn	ccg Pro	cgc	aac Asn 420	gtt Val	gte Val	gcc Ala	gcc Ala	gcg Ala 425	ctg Leu	ttg Leu	gca Ala	cgc Arg	aat Asn 430	gcc Ala	aac Asn	1296
cgc	Leu	ggc Gly 435	ttg Leu	caa Gln	cgc	aaa Lys	000 Pro 440	tgg Trp	gtg Val	aaa Lys	tot Ser	ccg Ser 445	ttt Phe	gcc Ala	Pro	1344
Glà aar	tca Ser 450	Lys	gta Val	gee Ala	gaa Glu	atc Ile 455	tat Tyr	rea	aaa Lys	gaæ Glu	gca Ala 460	gat Asp	Leu	Leu	ccc Pro	1392
gaa Glu 465	Met	gaa Glu	aaa Lys	ctc Leu	ggc Gly 470	ttc Phe	ggt Gly	atc Ile	gtt Val	gcc Ala 475	Phe	gca Ala	tgt Cys	acc Thr	acc Thr 480	1440
tgt Cys	aac Asn	ggc Gly	atg Met	agc Ser 485	Gly	gcg Ala	ctg	gat	ccg Pro 490	Lys	. atc	cag Gln	aaa Lys	gaa Glu 495	atc	1488
				ьeu					Val					Arg	aac Asn	1536
ttt Phe	gac Asp	ggo Gly 515	Arg	ato	cat His	ceg	tat Tyr 520	: Ala	aaa Lys	cag Glm	gct Ala	tto Phe 525	: Leu	gct Ala	tcg Ser	1584
cct Pro	cog Pro 530	Lev	gto Val	git Val	gco Ala	tac Tyr 535	Ala	ctg Lev	i Ala	ggc Gly	ago Ser 540	: Ile	cgt Arg	tto Phe	gat Asp	1632

att Ile 545	gaa Glu	aac Asn	gac Asp	gta Val	ctc Leu 550	ggc Gly	gtt Val	gca Ala	gac Asp	ggc Gly 555	aaa Lys	gaa Glu	atc Ile	cgc Arg	ctg Leu 560	1680
											gcc Ala					1728
											atc Ile					1776
											tac Tyr					1824
											gaa Glu 620					1872
											gcg Ala					1920
											gcg Ala					1968
											ttg Leu					2016
											ttg Leu					2064
											atg Met 700					2112
gac Asp 705	ggc Gly	agc Ser	gta Val	cgc Arg	caa Gln 710	ggt Gly	tcg Ser	ctg Leu	gca Ala	cgc Arg 715	gtt Val	gaa Glu	ccc Pro	gaa Glu	ggc Gly 720	2160
caa Gln	acc Thr	atg Met	cgc Arg	atg Met 725	tgg Trp	gaa Glu	gcc Ala	atc Ile	gaa Glu 730	acc Thr	t at Tyr	atg Met	aac Asn	cgc Arg 735	aaa Lys	2208
cag Gln	ccg Pro	ctc L eu	atc Ile 740	atc Ile	att Ile	gcc Ala	ggc	gcg Ala 745	gac Asp	tac Tyr	ggt Gly	caa Gln	ggc Gly 750	tca Ser	agc Ser	2256
											ggc Gly					2304
											aac Asn 780					2352

				aaa Lys				ctg Leu 800	2400
				tac Tyr				eeg Pro	2448
				att Ile				gtc Val	2496
				ctc Leu 840				gta Val	2544
				caa Gln				gaa Glu	2592
aac Asn	_	tag							2607

<211> 868

<212> PRT

<213> Neisseria menigitidis

<400> 73

Met Ala Ala Asn Gln Arg Tyr Arg Lys Pro Leu Pro Gly Thr Asp Leu 1 5 10 15

Glu Tyr Tyr Asp Ala Arg Ala Ala Cys Glu Gly Ile Lys Pro Gly Ser 20 25 30

Tyr Asp Lys Leu Pro Tyr Thr Ser Arg Ile Leu Ala Glu Asn Leu Val 35 40 45

Asn Arg Ala Asp Lys Val Asp Leu Pro Thr Leu Gln Ser Trp Leu Gly 50 60

Gln Leu Ile Glu Gly Lys Gln Glu Ile Asp Phe Pro Trp Tyr Pro Ala 65 70 75 80

Arg Val Val Cys His Asp Ile Leu Gly Gln Thr Ala Leu Val Asp Leu 85 90 95

Ala Gly Leu Arg Asp Ala Ile Ala Glu Lys Gly Gly Asp Pro Ala Lys
100 105 110

Val Asn Pro Val Val Gln Thr Gln Leu Ile Val Asp His Ser Leu Ala 115 120 125

Val Glu Cys Gly Gly Tyr Asp Pro Asp Ala Phe Arg Lys Asn Arg Glu 130 140

Ile Glu Asp Arg Arg Asn Glu Asp Arg Phe His Phe Ile Asn Trp Thr 145 150 155 160

- Lys Thr Ala Phe Glu Asn Val Asp Val Ile Pro Ala Gly Asn Gly Ile 165 170 175
- Met His Gln Ile Asn Leu Glu Lys Met Ser Pro Val Val Gln Val Lys 180 185 190
- Asn Gly Val Ala Phe Pro Asp Thr Cys Val Gly Thr Asp Ser His Thr 195 200 205
- Pro His Val Asp Ala Leu Gly Val Ile Ser Val Gly Val Gly Gly Leu 210 215 220
- Glu Ala Glu Thr Val Met Leu Gly Arg Ala Ser Met Met Arg Leu Pro 225 230 235 240
- Asp Ile Val Gly Val Glu Leu Asn Gly Lys Arg Lys Ala Gly Ile Thr 245 250 255
- Ala Thr Asp Ile Val Leu Ala Leu Thr Glu Phe Leu Arg Lys Glu Arg 260 265 270
- Val Val Gly Ala Phe Val Glu Phe Phe Gly Glu Gly Ala Arg Ser Leu 275 280 285
- Ser Ile Gly Asp Arg Ala Thr Ile Ser Asn Met Thr Pro Glu Phe Gly 290 295 300
- Ala Thr Ala Ala Met Phe Ala Ile Asp Glu Gln Thr Ile Asp Tyr Leu 305 310 315
- Lys Leu Thr Gly Arg Asp Asp Ala Gln Val Lys Leu Val Glu Thr Tyr 325 330 335
- Ala Lys Thr Ala Gly Leu Trp Ala Asp Ala Leu Lys Thr Ala Val Tyr 340 345 350
- Pro Arg Val Leu Lys Phe Asp Leu Ser Ser Val Thr Arg Asn Met Ala 355 360 365
- Gly Pro Ser Asn Pro His Ala Arg Phe Ala Thr Ala Asp Leu Ala Gly 370 375 380
- Lys Gly Leu Ala Lys Pro Tyr Glu Glu Pro Ser Asp Gly Gln Met Pro 385 390 395 400
- Asp Gly Ala Val Ile Ile Ala Ala Ile Thr Ser Cys Thr Asn Thr Ser 405 410 415
- Asn Pro Arg Asn Val Val Ala Ala Leu Leu Ala Arg Asn Ala Asn 420 425 430
- Arg Leu Gly Leu Gln Arg Lys Pro Trp Val Lys Ser Ser Phe Ala Pro 435 440 445
- Gly Ser Lys Val Ala Glu Ile Tyr Leu Lys Glu Ala Asp Leu Leu Pro 450 455 460
 - Glu Met Glu Lys Leu Gly Phe Gly Ile Val Ala Phe Ala Cys Thr Thr 465 470 475 480

- Cys Asn Gly Met Ser Gly Ala Leu Asp Pro Lys Ile Gln Lys Glu Ile 485 490 495
- Ile Asp Arg Asp Leu Tyr Ala Thr Ala Val Leu Ser Gly Asn Arg Asn 500 505
- Phe Asp Gly Arg Ile His Pro Tyr Ala Lys Gln Ala Phe Leu Ala Ser 515 520 525
- Pro Pro Leu Val Val Ala Tyr Ala Leu Ala Gly Ser Ile Arg Phe Asp 530 540
- Ile Glu Asn Asp Val Leu Gly Val Ala Asp Gly Lys Glu Ile Arg Leu 545 550 555 560
- Lys Asp Ile Trp Pro Thr Asp Clu Glu Ile Asp Ala Ile Val Ala Glu 565 570 575
- Tyr Val Lys Pro Gln Gln Phe Arg Asp Val Tyr Ile Pro Met Phe Asp 580 585 590
- Thr Gly Thr Ala Gln Lys Ala Pro Ser Pro Leu Tyr Asp Trp Arg Pro 595 600 605
- Met Ser Thr Tyr Ile Arg Arg Pro Pro Tyr Trp Glu Gly Ala Leu Ala 610 615 620
- Gly Glu Arg Thr Leu Ser Gly Met Arg Pro Leu Ala Ile Leu Pro Asp 625 630 635
- Asn Ile Thr Thr Asp His Leu Ser Pro Ser Asn Ala Ile Leu Ala Ser 645 650 655
- Ser Ala Ala Gly Glu Tyr Leu Ala Lys Met Gly Leu Pro Glu Glu Asp
 660 665 670
- Phe Asn Ser Tyr Ala Thr His Arg Gly Asp His Leu Thr Ala Gln Arg 675 680 685
- Ala Thr Phe Ala Asn Pro Lys Leu Phe Asn Glu Met Val Arg Asn Glu 690 695 700
- Asp Gly Ser Val Arg Gln Gly Ser Leu Ala Arg Val Glu Pro Glu Gly 705 710 715 720
- Gln Thr Met Arg Met Trp Glu Ala Ile Glu Thr Tyr Met Asn Arg Lys 725 730 735
- Gin Pro Leu Ile Ile Ile Ala Gly Ala Asp Tyr Gly Gln Gly Ser Ser 740 745 750
- Arg Asp Trp Ala Ala Lys Gly Val Arg Leu Ala Gly Val Glu Ala Ile 755 760 765
- Val Ala Glu Gly Phe Glu Arg Ile His Arg Thr Asn Leu Ile Gly Met 770 780
- Gly Val Leu Pro Leu Gln Phe Lys Pro Gly Thr Asn Arg His Thr Leu 785 790 795 800

Gln Leu Asp Gly Thr Glu Thr Tyr Asp Val Val Gly Glu Arg Thr Pro 805 810 815

Arg Cys Asp Leu Thr Leu Val Ile His Arg Lys Asn Gly Glu Thr Val 820 825 830

Glu Val Pro Ile Thr Cys Arg Leu Asp Thr Ala Glu Glu Val Leu Val 835 840 845

Tyr Glu Ala Gly Gly Val Leu Gln Arg Phe Ala Gln Asp Phe Leu Glu 850 860

Gly Asn Ala Ala 865

<210> 74

<211> 1170

<212> DNA

<213> Neisseria menigitidis

<220>

<221> CDS

<222> (1)..(1167)

<400> 74

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Met Pro Gln Ile Lys Ile Pro Ala Val Tyr Tyr Arg Gly Gly Thr Ser
1 5 10 15

aaa ggc gtg ttt ttc aaa cgt tcc gac ctg ccc gag gcg gcg cgg gaa 96 Lys Gly Val Phe Phe Lys Arg Ser Asp Leu Pro Glu Ala Ala Arg Glu 20 25 30

909 99a ago goa cgo gao aaa ato oto ttg cgo gta oto ggo ago ccg 144 Ala Gly Ser Ala Arg Asp Lys Ile Leu Leu Arg Val Leu Gly Ser Pro 35 40 45

gat ccc tac ggc aag cag ata gac ggt ttg ggc aac gcc agc tcg tcc 192 Asp Pro Tyr Gly Lys Gln Ile Asp Gly Leu Gly Asn Ala Ser Ser Ser 50 55

acc agc aag geg gtg att ttg gac aag tcc gaa egc gec gat cac gat 240 Thr Ser Lys Ala Val Ile Leu Asp Lys Ser Glu Arg Ala Asp His Asp 65 70 80

gtc gat tac ctt ttc ggg caa gtt tcc atc gac aaa cct ttt gtc gat 288 Val Asp Tyr Leu Phe Gly Gln Val Ser Ile Asp Lys Pro Phe Val Asp 85 90 95

tgg agt ggc aac tgc ggc aac ctc acc gcc gcc gtg ggc gca ttt gcc 336
Trp Ser Gly Asn Cys Gly Asn Leu Thr Ala Ala Val Gly Ala Phe Ala
100 105 110

atc gag caa ggc ttg gtc gat aaa ggc aag att cct tca gac ggc atc 384
Ile Glu Gln Gly Leu Val Asp Lys Gly Lys Ile Pro Ser Asp Gly Ile
115 120 125

											aaa Lys 140					432
											aca Thr					480
											caa Gln					528
		_	_		_		_	_			acc Thr			_	-	576
											aaa Lys					624
											gcc Ala 220					672
											gat Asp					720
											ctg Leu					768
											cac His					816
gcc Ala	ttc Phe	gtc Val 275	gcg Ala	CCC Pro	gcc Ala	gcc Ala	gat Asp 280	tac Tyr	acc Thr	gcc Ala	tcc Ser	agt Ser 285	ggc Gly	aaa Lys	acc Thr	864
											gcc Ala 300					912
											gtt Val					960
											gcc Ala					1008
acg Thr	cgt Arg	Lys	gaa Glu 340	gtg Val	cgc Arg	ttc Phe	gjå aaa	cat His 345	cct Pro	tcc Ser	ggc	aca Thr	ttg Leu 350	cgc Arg	gtc Val	1056
											acg Thr		Thr		gcg Ala	1104
gtt Val	atg Met 370	agc Ser	cgc Arg	agc Ser	gca Ala	cgc Arg 375	gtg Val	atg Met	atg Met	Glu	ggt Gly 380	tgg (Trp	gtc (Val)	agg 9 Arg 1	gtg Val	1152
	gaa Glu				taa											1170

- <210> 75
- <211> 389
- <212> PRT
- <213> Neisseria menigitidis

<400> 75

Met Pro Gln Ile Lys Ile Pro Ala Val Tyr Tyr Arg Gly Gly Thr Ser

Lys Gly Val Phe Phe Lys Arg Ser Asp Leu Pro Glu Ala Ala Arg Glu 20 25 30

Ala Gly Ser Ala Arg Asp Lys Ile Leu Leu Arg Val Leu Gly Ser Pro 35 40 45

Asp Pro Tyr Gly Lys Gln Ile Asp Gly Leu Gly Asn Ala Ser Ser Ser 50 55 60

Thr Ser Lys Ala Val Ile Leu Asp Lys Ser Glu Arg Ala Asp His Asp 65 70 75 80

Val Asp Tyr Leu Phe Gly Gln Val Ser Ile Asp Lys Pro Phe Val Asp 85 90 95

Trp Ser Gly Asn Cys Gly Asn Leu Thr Ala Ala Val Gly Ala Phe Ala 100 105 110

Ile Glu Gln Gly Leu Val Asp Lys Gly Lys Ile Pro Ser Asp Gly Ile 115 120 125

Cys Thr Val Lys Ile Trp Gln Lys Asn Ile Gly Lys Thr Ile Ile Ala 130 135 140

His Val Pro Met Gln Asn Gly Ala Val Leu Glu Thr Gly Asp Phe Glu 145 150 155 160

Leu Asp Gly Val Thr Phe Pro Ala Ala Glu Val Gln Ile Glu Phe Leu 165 170 175

Asp Pro Ala Asp Gly Glu Gly Ser Met Phe Pro Thr Gly Asn Leu Val

Asp Glu Ile Asp Val Pro Asn Ile Gly Arg Leu Lys Ala Thr Leu Ile 195 200 205

Asn Ala Gly Ile Pro Thr Val Phe Leu Asn Ala Ala Asp Leu Gly Tyr 210 215 220

Thr Gly Lys Glu Leu Gln Asp Asp Ile Asn Asn Asp Ala Ala Ala Leu 225 230 235 240 Glu Lys Phe Glu Lys Ile Arg Ala Tyr Gly Ala Leu Lys Met Gly Leu 245 250 255

Ile Ser Asp Val Ser Glu Ala Ala Ala Arg Ala His Thr Pro Lys Val 260 265 270

Ala Phe Val Ala Pro Ala Ala Asp Tyr Thr Ala Ser Ser Gly Lys Thr 275 280 285

Val Asn Ala Ala Asp Ile Asp Leu Val Arg Ala Leu Ser Met Gly 290 295 300

Lys Leu His His Ala Met Met Gly Thr Ala Ser Val Ala Ile Ala Thr 305 310 315

Ala Ala Val Pro Cly Thr Leu Val Asn Leu Ala Ala Gly Gly Gly 325 330 335

Thr Arg Lys Glu Val Arg Phe Gly His Pro Ser Gly Thr Leu Arg Val 340 345 350

Gly Ala Ala Glu Cys Gln Asp Gly Gln Trp Thr Ala Thr Lys Ala 355 360 365

Val Met Ser Arg Ser Ala Arg Val Met Met Glu Gly Trp Val Arg Val 370 380

Pro Glu Asp Cys Phe 385

<210> 76

<211> 2094

<212> DNA

<213> Neisseria gonorrhoeae

<220>

<221> CDS

<222> (1)..(2091)

<400> 76

atg aat tcg acc gca agt aaa acc ctg aaa gga ttg tcg ctg gtg ttt 48
Met Asn Ser Thr Ala Ser Lys Thr Leu Lys Gly Leu Ser Leu Val Phe

tte gee tet gge tte tge gee etg att tae eag gte age tgg eag agg 96
Phe Ala Ser Gly Phe Cys Ala Leu Ile Tyr Gln Val Ser Trp Gln Arg

ctt cta ttc agc cac ata ggt atc gat ttg agt tcg att act gtc att Leu Leu Phe Ser His Ile Gly Ile Asp Leu Ser Ser Ile Thr Val Ile
35 40 45

att tot gta tot atg gto ggo tot ggt gta ggt gcg tat tot ggo gga 192 Tle Ser Val Phe Met Val Gly Leu Gly Val Gly Ala Tyr Phe Gly Gly

cgc att gct gac cgt ttt cct tca agt atc atc ccc ctg ttt tgc atc 240 Arg Ile Ala Asp Arg Phe Pro Ser Ser Ile Ile Pro Leu Phe Cys Ile

65					70					75					80	
gct Ala	gaa Glu	gta Val	tcc Ser	atc Ile 85	ggt Gly	ctg Leu	ttc Phe	ggt Gly	ttg Leu 90	gta Val	agc Ser	aag Lys	ggt Gly	ctg Leu 95	att Ile	288
tcc Ser	GJA āāc	ttg Leu	999 Gly 100	cat Hıs	ctt Leu	tta Leu	gtt Val	gag Glu 105	gct Ala	gat Asp	ttg Leu	ccc Pro	atc Ile 110	atc Ile	gct Ala	336
gct Ala	gcc Ala	aat Asn 115	ttc Phe	ctc Leu	tta Leu	ttg Leu	ctg Leu 120	ctt Leu	cct Pro	acc Thr	ttt Phe	atg Met 125	atg Met	gg¢ Gly	gcg Ala	384
acc Thr	ttg Leu 130	ccc Pro	ttg Leu	ctg Leu	acc Thr	tgt Cys 135	ttt Phe	ttt Phe	aac Asn	cgg Arg	aaa Lys 140	ata Ile	cat His	aat Asn	gtt Val	432
ggc Gly 145	gag Glu	tct Ser	atc Ile	ggt Gly	acc Thr 150	tta Leu	tat Tyr	ttt Phe	ttc Phe	aac Asn 155	act Thr	ttg Leu	ggt Gly	Ala	gca Ala 160	480
ctc Leu	gga Gly	tcg Ser	ctt Leu	gcc Ala 165	gcc Ala	gcc Ala	gaa Glu	ttt Phe	ttc Phe 170	tac Tyr	gtc Val	ttt Phe	ttt Phe	acc Thr 175	ctc Leu	528
tcc Ser	caa Gln	acc Thr	att Ile 180	gcg Ala	ctg Leu	aca Thr	gcc Ala	tgc Cys 185	ctt Leu	aac Asn	ctt Leu	ctg Leu	att Ile 190	gct Ala	gct Ala	576
tca Ser	gta Val	tgc Cys 195	tgc Cys	gtt Val	aca Thr	gaa Glu	agg Arg 200	atg Met	gat Asp	atg Met	gtg Val	aac Asn 205	act Thr	aaa Lys	ccg Pro	624
aat Asn	act Thr 210	ser	gtg Val	att Ile	aat Asn	atg Met 215	ctt Leu	tct Ser	ttc Phe	ctt Leu	acc Thr 220	gga Gly	tta Leu	ttg Leu	agc Ser	672
ttg Leu 225	. Gly	ata Ile	gaa Glu	gtc Val	ttg Leu 230	tgg Trp	gta Val	agg Arg	atg Met	ttt Phe 235	Ser	ttc Phe	gca Ala	gca Ala	cag Gln 240	720
tcc Ser	gtg Val	cct Pro	cag Gln	gca Ala 245	Phe	tca Ser	ttt Phe	att Ile	ctt Leu 250	Ala	tgt Cys	ttt Phe	ctg Leu	acc Thr 255	ggt	768
ato Ile	gcc Ala	gtc Val	ggc Gly 260	Ala	tat Tyr	ttt Phe	ggc	aaa Lys 265	Arc	att Ile	tgc Cys	cgo Arg	ago Ser 270	Arç	ttt Phe	816
gtt Val	gat Asp	att Ile 275	Pro	ttt Phe	atc : Ile	ggg	cag Gln 280	. Cys	tto Phe	ttg Lev	tgg Trp	gc9 Ala 285	Gly	att Ile	gcc Ala	864
gat Asp	ttt Phe 290	Leu	att Ile	ttg Leu	ggt Gly	gct Ala 295	Ala	j tgg L Trp	tte Lei	g ttg 1 Lev	acc Thr	: Gly	ttt Phe	tce Ser	ggt Gly	912
tt: Ph	gto val	cac l His	cac His	gcc Ala	ggt Gly	att	tto Pho	att E Ile	aco Th:	c cto r Lev	j tct i Sei	gco Ala	gto a Val	gto Val	e agg l Arg	960

305 315 320 310 ggg ttg att ttc cca ctt gta cac cat gtg ggt acg gat ggc aac aaa Gly Leu Ile Phe Pro Leu Val His His Val Gly Thr Asp Gly Asn Lys 325 too gga cga cag gtt too aat gtt tat tto gcc aac gtt gcc ggc agt Ser Gly Arg Gln Val Ser Asn Val Tyr Phe Ala Asn Val Ala Gly Ser gca ttg ggt ccg gtc ctt atc ggc ttt gtg ata ctt gat ttg ttc 1104 Ala Leu Gly Pro Val Leu Ile Gly Phe Val Ile Leu Asp Leu Leu Ser 355 360 acc caa cag att tac ctg ctc atc tgt ttg att tct gct gct gtc cct 1152 Thr Gln Gln Ile Tyr Leu Leu Ile Cys Leu Ile Ser Ala Ala Val Pro ttg ttt tgt aca ctg ttc caa aaa agt ctc cga ctg aat gca gtg tcg Leu Phe Cys Thr Leu Phe Gln Lys Ser Leu Arg Leu Asn Ala Val Ser 385 395 gta gca gtt tee eta atg tte gge ate ete atg tte eta etg eeg gat 1248 Val Ala Val Ser Leu Met Phe Gly Ile Leu Met Phe Leu Leu Pro Asp 405 410 tot gto ttt caa aat att got ggo ogt oog gat agg ttg att gaa aac 1296 Ser Val Phe Gln Asn Ile Ala Gly Arg Pro Asp Arg Leu Ile Glu Asn 420 425 aaa cac ggc att gtt gcg gtt tac cat aga gat ggt gat aag gtt gtt 1344 Lys His Gly Ile Val Ala Val Tyr His Arg Asp Gly Asp Lys Val Val tat ggg gcg aat gta tac gac ggc gca tac aat acc gat ata ttc aat 1392 Tyr Gly Ala Asn Val Tyr Asp Gly Ala Tyr Asn Thr Asp Ile Phe Asn agt gtc aac ggc atc gas cgt gcc tat ctg cta ccc tcc ctg aag tcc 1440 Ser Val Asn Gly Ile Glu Arg Ala Tyr Leu Leu Pro Ser Leu Lys Ser 475 470 1488 ggc ata ege ege att the gte gtt gga ttg agt aca ggt teg tgg geg Gly Ile Arg Arg Ile Phe Val Val Gly Leu Ser Thr Gly Ser Trp Ala ege gte tig tet gee att eeg gaa atg eag teg atg ate gtt geg gaa 1536 Arg Val Leu Ser Ala Ile Pro Glu Met Gln Ser Met Ile Val Ala Glu 500 505 510 atc aat ccg gca tac cgt agc ctt atc gcg gac gag ccg caa atc gca 1584 Ile Asn Pro Ala Tyr Arg Ser Leu Ile Ala Asp Glu Pro Gln Ile Ala 520 cog oft ttg cag gac aaa cgt gtt gaa att gta ttg gat gac ggt agg 1632 Pro Leu Gln Asp Lys Arg Val Glu Ile Val Leu Asp Asp Gly Arg asa tgg ctg cgt cgc cat cct gat gaa asa ttc gac ctg att ttg atg 1680 Lys Trp Leu Arg Arg His Pro Asp Glu Lys Phe Asp Leu Ile Leu Met

545	550	555	560
Asn Ser Thr Trp T		tat tcc act aac c Tyr Ser Thr Asn I 570	
gaa ttt tta aaa c Glu Phe Leu Lys G 580	ag gtg caa agc In Val Gln Ser	cac ctt acc ccg g His Leu Thr Pro A 585	gat ggt att gta 1776 ssp Gly Ile Val 590
atg ttt aat acc a Met Phe Asn Thr T 595		His Ala Phe Ala T	
agt att ccc tat g Ser Ile Pro Tyr A 610	_	ggg cat atg gta g Gly His Met Val V 620	
		gaa ctg ctc aag c Glu Leu Leu Lys 6 635	
Arg Leu Ile Trp P		agg cac gta ttt g Arg His Val Phe A 650	
		gtc tct cgt atg o Val Ser Arg Met I 665	
		gtc att act gac g Val Ile Thr Asp A	
gta gaa tac aaa t Val Glu Tyr Lys T 690			2094

<211> 697

<212> PRT

<213> Neisseria gonorrhoeae

<400> 77

Met Asn Ser Thr Ala Ser Lys Thr Leu Lys Gly Leu Ser Leu Val Phe 1 $$ 5 $$ 10 $$ 15

Phe Ala Ser Gly Phe Cys Ala Leu Ile Tyr Gln Val Ser Trp Gln Arg 20 25 30

Leu Leu Phe Ser His Ile Gly Ile Asp Leu Ser Ser Ile Thr Val Ile $35 \hspace{1cm} 40 \hspace{1cm} 45$

Ile Ser Val Phe Met Val Gly Leu Gly Val Gly Ala Tyr Phe Gly Gly 50 55 60

Arg Ile Ala Asp Arg Phe Pro Ser Ser Ile Ile Pro Leu Phe Cys Ile 65 70 75 80

- Ala Glu Val Ser Ile Gly Leu Phe Gly Leu Val Ser Lys Gly Leu Ile 85 90 95
- Ser Gly Leu Gly His Leu Leu Val Glu Ala Asp Leu Pro Ile Ile Ala 100 105 110
- Ala Ala Asn Phe Leu Leu Leu Leu Pro Thr Phe Met Met Gly Ala 115 120 125
- Thr Leu Pro Leu Leu Thr Cys Phe Phe Asn Arg Lys Ile His Asn Val
- Gly Glu Ser Ile Gly Thr Leu Tyr Phe Phe Asn Thr Leu Gly Ala Ala 145 150 150
- Leu Gly Ser Leu Ala Ala Glu Phe Phe Tyr Val Phe Phe Thr Leu 165 170 175
- Ser Gln Thr Ile Ala Leu Thr Ala Cys Leu Asn Leu Leu Ile Ala Ala 180 185 190
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- Val Ala Val Ser Leu Met Phe Gly Ile Leu Met Phe Leu Leu Pro Asp 405 410 415
- Ser Val Phe Gln Asn Ile Ala Gly Arg Pro Asp Arg Leu Ile Glu Asn 420 425 430
- Lys His Gly Ile Val Ala Val Tyr His Arg Asp Gly Asp Lys Val Val 435 440 445
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- Lys Trp Leu Arg Arg His Pro Asp Glu Lys Phe Asp Leu Ile Leu Met \$45 \$50 \$55 \$560
- Asn Ser Thr Trp Tyr Trp Arg Ala Tyr Ser Thr Asn Leu Leu Ser Ala 565 570 575
- Glu Phe Leu Lys Gln Val Gln Ser His Leu Thr Pro Asp Gly Ile Val
- Met Phe Asn Thr Thr His Ser Pro His Ala Phe Ala Thr Ala Val His 595 600 605
- Ser Ile Pro Tyr Ala Tyr Arg Tyr Gly His Met Val Val Gly Ser Ala 610 615 620
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